

Figure 1: Nucleotide and deduced amino acid sequence of CPN100634

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gataaaaatt cttgacagct gttttgtcat ctttaacttg atttacttat tttgtttcta 60
tattgatgcg aatagttctc taaaaaaca aagcattacc atg aag act tcg att 115
                                         Met Lys Thr Ser Ile
                                         1           5

cct tgg gtt tta gtt tcc tcc gtg tta gct ttc tca tgt cac cta cag 163
Pro Trp Val Leu Val Ser Ser Val Leu Ala Phe Ser Cys His Leu Gln
              10              15              20

tca cta gct aac gag gaa ctt tta tca cct gat gat agc ttt aat gga 211
Ser Leu Ala Asn Glu Glu Leu Leu Ser Pro Asp Asp Ser Phe Asn Gly
              25              30              35

aat atc gat tca gga acg ttt act cca aaa act tca gcc aca aca tat 259
Asn Ile Asp Ser Gly Thr Phe Thr Pro Lys Thr Ser Ala Thr Thr Tyr
              40              45              50

tct cta aca gga gat gtc ttc ttt tac gag cct gga aaa ggc act ccc 307
Ser Leu Thr Gly Asp Val Phe Phe Tyr Glu Pro Gly Lys Gly Thr Pro
              55              60              65

tta tct gac agt tgt ttt aag caa acc acg gac aat ctt acc ttc ttg 355
Leu Ser Asp Ser Cys Phe Lys Gln Thr Thr Asp Asn Leu Thr Phe Leu
              70              75              80              85

ggg aac ggt cat agc tta acg ttt ggc ttt ata gat gct ggc act cat 403
Gly Asn Gly His Ser Leu Thr Phe Gly Phe Ile Asp Ala Gly Thr His
              90              95              100

gca ggt gct gct gca tct aca aca gca aat aag aat ctt acc ttc tca 451
Ala Gly Ala Ala Ala Ser Thr Thr Ala Asn Lys Asn Leu Thr Phe Ser
              105              110              115

ggg ttt tcc tta ctg agt ttt gat tcc tct cct agc aca acg gtt act 499
Gly Phe Ser Leu Leu Ser Phe Asp Ser Ser Pro Ser Thr Thr Val Thr
              120              125              130

aca ggt cag gga acg ctt tcc tca gca gga ggc gta aat tta gaa aat 547
Thr Gly Gln Gly Thr Leu Ser Ser Ala Gly Gly Val Asn Leu Glu Asn
              135              140              145

att cgt aaa ctt gta gtt gct ggg aat ttt tct act gca gat ggt gga 595
Ile Arg Lys Leu Val Val Ala Gly Asn Phe Ser Thr Ala Asp Gly Gly
              150              155              160              165

gct atc aaa gga gcg tct ttc ctt tta act ggc act tct gga gat gct 643
Ala Ile Lys Gly Ala Ser Phe Leu Leu Thr Gly Thr Ser Gly Asp Ala
              170              175              180

ctt ttt agt aac aac tct tca tca aca aag gga gga gca att gct act 691
Leu Phe Ser Asn Asn Ser Ser Ser Thr Lys Gly Gly Ala Ile Ala Thr
              185              190              195

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Fig. 1 (con't)

aca gca ggc gct cgc ata gca aat aac aca ggt tat gtt aga ttc cta Thr Ala Gly Ala Arg Ile Ala Asn Asn Thr Gly Tyr Val Arg Phe Leu 200 205 210	739
tct aac ata gcg tct acg tca gga ggc gct atc gat gat gaa ggc acg Ser Asn Ile Ala Ser Thr Ser Gly Gly Ala Ile Asp Asp Glu Gly Thr 215 220 225	787
tcg ata cta tcg aac aac aaa ttt cta tat ttt gaa ggg aat gca gcg Ser Ile Leu Ser Asn Asn Lys Phe Leu Tyr Phe Glu Gly Asn Ala Ala 230 235 240 245	835
aaa act act ggc ggt gcg atc tgc aac acc aag gcg agt gga tct cct Lys Thr Thr Gly Gly Ala Ile Cys Asn Thr Lys Ala Ser Gly Ser Pro 250 255 260	883
gaa ctg ata atc tct aac aat aag act ctg atc ttt gct tca aac gta Glu Leu Ile Ile Ser Asn Asn Lys Thr Leu Ile Phe Ala Ser Asn Val 265 270 275	931
gca gaa aca agc ggt ggc gcc atc cat gct aaa aag cta gcc ctt tcc Ala Glu Thr Ser Gly Gly Ala Ile His Ala Lys Lys Leu Ala Leu Ser 280 285 290	979
tct gga ggc ttt aca gag ttt cta cga aat aat gtc tca tca gca act Ser Gly Gly Phe Thr Glu Phe Leu Arg Asn Asn Val Ser Ser Ala Thr 295 300 305	1027
cct aag ggg ggt gct atc agc atc gat gcc tca gga gag ctc agt ctt Pro Lys Gly Gly Ala Ile Ser Ile Asp Ala Ser Gly Glu Leu Ser Leu 310 315 320 325	1075
tct gca gag aca gga aac att acc ttt gta aga aat acc ctt aca aca Ser Ala Glu Thr Gly Asn Ile Thr Phe Val Arg Asn Thr Leu Thr Thr 330 335 340	1123
acc gga agt acc gat act cct aaa cgt aat gcg atc aac ata gga agt Thr Gly Ser Thr Asp Thr Pro Lys Arg Asn Ala Ile Asn Ile Gly Ser 345 350 355	1171
aac ggg aaa ttc acg gaa tta cgg gct gct aaa aat cat aca att ttc Asn Gly Lys Phe Thr Glu Leu Arg Ala Ala Lys Asn His Thr Ile Phe 360 365 370	1219
ttc tat gat ccc atc act tca gaa gga acc tca tca gac gta ttg aag Phe Tyr Asp Pro Ile Thr Ser Glu Gly Thr Ser Ser Asp Val Leu Lys 375 380 385	1267
ata aat aac ggc tct gcg gga gct ctc aat cca tat caa gga acg att Ile Asn Asn Gly Ser Ala Gly Ala Leu Asn Pro Tyr Gln Gly Thr Ile 390 395 400 405	1315
cta ttt tct gga gaa acc cta aca gca gat gaa ctt aaa gtt gct gac Leu Phe Ser Gly Glu Thr Leu Thr Ala Asp Glu Leu Lys Val Ala Asp 410 415 420	1363

Fig. 1 (con't)

aat tta aaa tct tca ttc acg cag cca gtc tcc cta tcc gga gga aag	1411
Asn Leu Lys Ser Ser Phe Thr Gln Pro Val Ser Leu Ser Gly Gly Lys	
425 430 435	
tta ttg cta caa aag gga gtc act tta gag agc acg agc ttc tct caa	1459
Leu Leu Leu Gln Lys Gly Val Thr Leu Glu Ser Thr Ser Phe Ser Gln	
440 445 450	
gag gcc ggt tct ctc ctc ggc atg gat tca gga acg aca tta tca act	1507
Glu Ala Gly Ser Leu Leu Gly Met Asp Ser Gly Thr Thr Leu Ser Thr	
455 460 465	
aca gct ggg agt att aca atc acg aac cta gga atc aat gtt gac tcc	1555
Thr Ala Gly Ser Ile Thr Ile Thr Asn Leu Gly Ile Asn Val Asp Ser	
470 475 480 485	
tta ggt ctt aag cag ccc gtc agc cta aca gca aaa ggt gct tca aat	1603
Leu Gly Leu Lys Gln Pro Val Ser Leu Thr Ala Lys Gly Ala Ser Asn	
490 495 500	
aaa gtg atc gta tct ggg aag ctc aac ctg att gat att gaa ggg aac	1651
Lys Val Ile Val Ser Gly Lys Leu Asn Leu Ile Asp Ile Glu Gly Asn	
505 510 515	
att tat gaa agt cat atg ttc agc cat gac cag ctc ttc tct cta tta	1699
Ile Tyr Glu Ser His Met Phe Ser His Asp Gln Leu Phe Ser Leu Leu	
520 525 530	
aaa atc acg gtt gat gct gat gtt gat act aac gtt gac atc agc agc	1747
Lys Ile Thr Val Asp Ala Asp Val Asp Thr Asn Val Asp Ile Ser Ser	
535 540 545	
ctt atc cct gtt cct gct gag gat cct aat tca gaa tac gga ttc caa	1795
Leu Ile Pro Val Pro Ala Glu Asp Pro Asn Ser Glu Tyr Gly Phe Gln	
550 555 560 565	
gga caa tgg aat gtt aat tgg act acg gat aca gct aca aat aca aaa	1843
Gly Gln Trp Asn Val Asn Trp Thr Thr Asp Thr Ala Thr Asn Thr Lys	
570 575 580	
gag gcc acg gca act tgg acc aaa aca gga ttt gtt ccc agc ccc gaa	1891
Glu Ala Thr Ala Thr Trp Thr Lys Thr Gly Phe Val Pro Ser Pro Glu	
585 590 595	
aga aaa tct gcg tta gta tgc aat acc cta tgg gga gtc ttt act gac	1939
Arg Lys Ser Ala Leu Val Cys Asn Thr Leu Trp Gly Val Phe Thr Asp	
600 605 610	
att cgc tct ctg caa cag ctt gta gag atc ggc gca act ggt atg gaa	1987
Ile Arg Ser Leu Gln Gln Leu Val Glu Ile Gly Ala Thr Gly Met Glu	
615 620 625	
cac aaa caa ggt ttc tgg gtt tcc tcc atg acg aac ttc ctg cat aac	2035
His Lys Gln Gly Phe Trp Val Ser Ser Met Thr Asn Phe Leu His Lys	
630 635 640 645	

Fig. 1 (con't)

act gga gat gaa aat cgc aaa ggc ttc cgt cat acc tct gga ggc tac	2083
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650 655 660	
gtc atc ggt gga agt gct cac act cct aaa gac gac cta ttt acc ttt	2131
Val Ile Gly Gly Ser Ala His Thr Pro Lys Asp Asp Leu Phe Thr Phe	
665 670 675	
gcg ttc tgc cat ctc ttt gct aga gac aaa gat tgt ttt atc gct cac	2179
Ala Phe Cys His Leu Phe Ala Arg Asp Lys Asp Cys Phe Ile Ala His	
680 685 690	
aac aac tct aga acc tac ggt gga act tta ttc ttc aag cac tct cat	2227
Asn Asn Ser Arg Thr Tyr Gly Gly Thr Leu Phe Phe Lys His Ser His	
695 700 705	
acc cta caa ccc caa aac tat ttg aga tta gga aga gca aag ttt tct	2275
Thr Leu Gln Pro Gln Asn Tyr Leu Arg Leu Gly Arg Ala Lys Phe Ser	
710 715 720 725	
gaa tca gct ata gaa aaa ttc cct agg gaa att ccc cta gcc ttg gat	2323
Glu Ser Ala Ile Glu Lys Phe Pro Arg Glu Ile Pro Leu Ala Leu Asp	
730 735 740	
gtc caa gtt tcg ttc agc cat tca gac aac cgt atg gaa acg cac tat	2371
Val Gln Val Ser Phe Ser His Ser Asp Asn Arg Met Glu Thr His Tyr	
745 750 755	
acc tca ttg cca gaa tcc gaa ggt tct tgg agc aac gag tgt ata gct	2419
Thr Ser Leu Pro Glu Ser Glu Gly Ser Trp Ser Asn Glu Cys Ile Ala	
760 765 770	
ggt ggt atc ggc cta gac ctt cct ttt gtt ctt tcc aac cca cat cct	2467
Gly Gly Ile Gly Leu Asp Leu Pro Phe Val Leu Ser Asn Pro His Pro	
775 780 785	
ctt ttc aag acc ttc att cca cag atg aaa gtc gaa atg gtt tat gta	2515
Leu Phe Lys Thr Phe Ile Pro Gln Met Lys Val Glu Met Val Tyr Val	
790 795 800 805	
tca caa aat agc ttc ttc gaa agc tct agt gat ggc cgt ggt ttt agt	2563
Ser Gln Asn Ser Phe Phe Glu Ser Ser Ser Asp Gly Arg Gly Phe Ser	
810 815 820	
att gga agg ctg ctt aac ctc tcg att cct gtg ggt gcg aaa ttc gtg	2611
Ile Gly Arg Leu Leu Asn Leu Ser Ile Pro Val Gly Ala Lys Phe Val	
825 830 835	
cag ggg gat atc gga gat tcc tac acc tat gat ctc tca gga ttc ttt	2659
Gln Gly Asp Ile Gly Asp Ser Tyr Thr Tyr Asp Leu Ser Gly Phe Phe	
840 845 850	
gtt tcc gat gtc tat cgt aac aat ccc caa tct aca gcg act ctt grg	2707
Val Ser Asp Val Tyr Arg Asn Asn Pro Gln Ser Thr Ala Thr Leu Val	
855 860 865	

Fig. 1 (con't)

atg agc cca gac tct tgg aaa att cgc ggt ggc aat ctt tca aga cag	2755
Met Ser Pro Asp Ser Trp Lys Ile Arg Gly Gly Asn Leu Ser Arg Gln	
870	885
gca ttt tta ctg agg ggt agc aac aac tac gtc tac aac tcc aat tgt	2803
Ala Phe Leu Leu Arg Gly Ser Asn Asn Tyr Val Tyr Asn Ser Asn Cys	
890	900
gag ctc ttc gga cat tac gct atg gaa ctc cgt gga tct tca agg aac	2851
Glu Leu Phe Gly His Tyr Ala Met Glu Leu Arg Gly Ser Ser Arg Asn	
905	915
tac aat gta gat gtt ggt acc aaa ctc cga ttc tagattgcta aaactcccta	2904
Tyr Asn Val Asp Val Gly Thr Lys Leu Arg Phe	
920	925
gttcttctag ggagttttct catactttta gggaaatatt tgctat	2950

Figure 2: Restriction enzyme analysis of CPN100624

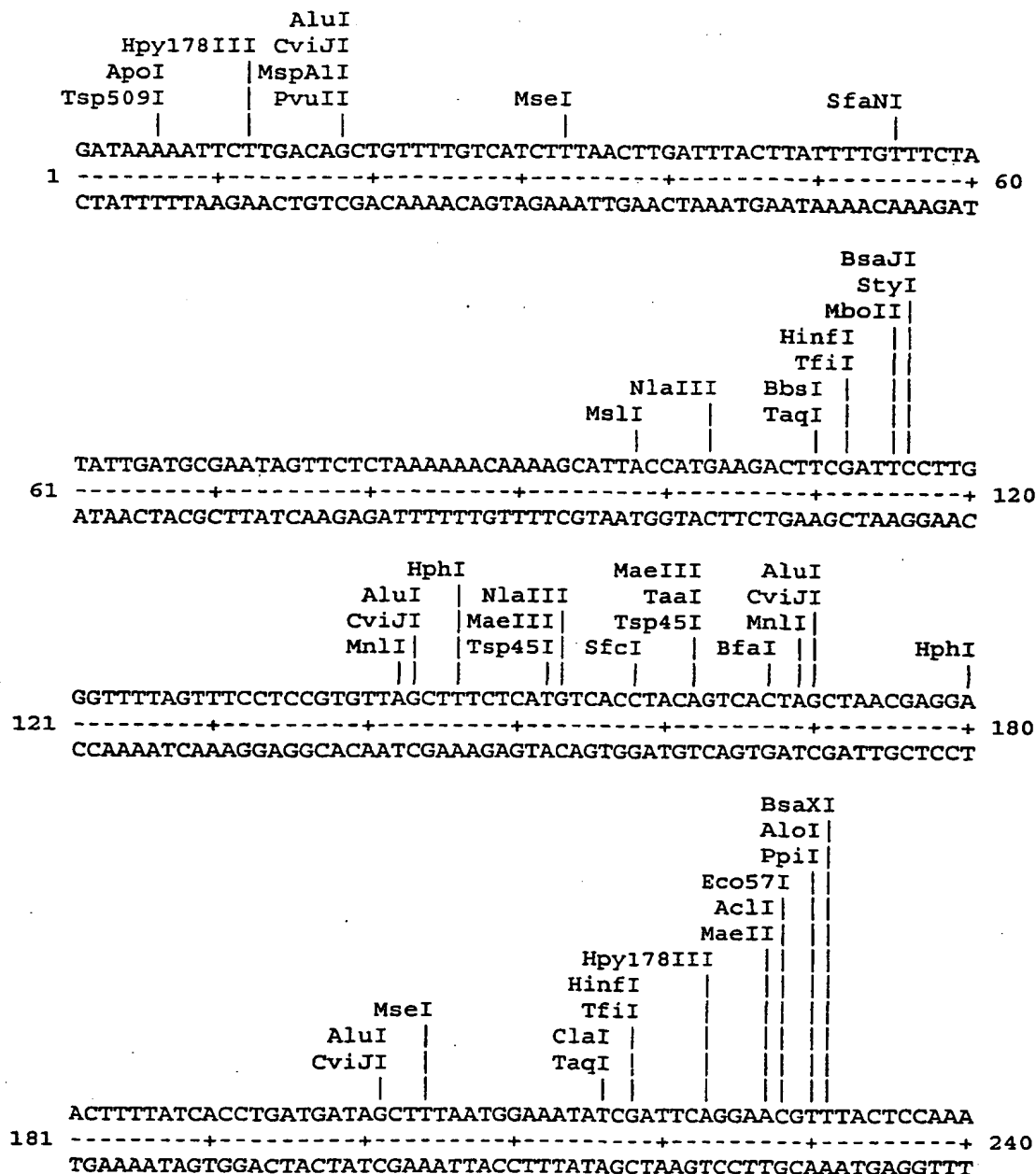
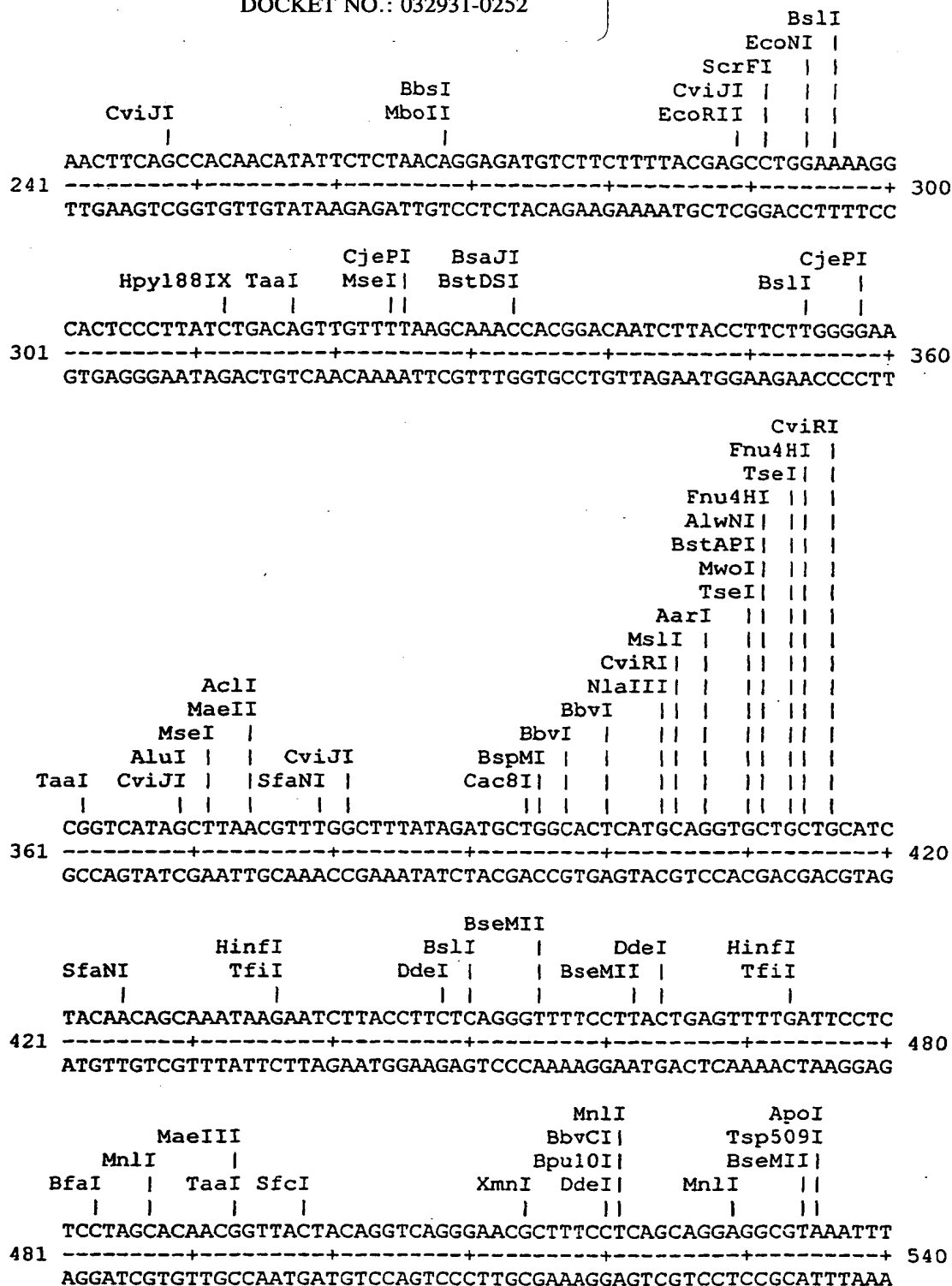


Fig. 2 (con't)

Title: CHLAMYDIA ANTIGEN AND  
CORRESPONDING DNA  
FRAGMENTS AND USES THEREOF  
Inventor(s): Andrew D. MURDIN et al.  
DOCKET NO.: 032931-0252



SspI  
 XmnI  
 ApoI  
 CjeI  
 Tsp509I  
 PstI  
 CviRI  
 SfcI  
 BccI  
 HgaI  
 AluI  
 CviJI  
 541  
 AGAAAAATATTCGTAAACTTGTAGTTGCTGGGAATTTTCTACTGCAGATGGTGGAGCTAT  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600  
 TCTTTTATAAGCATTTGAACATCAACGACCCTTAAAAAGATGACGTCTACCACCTCGATA  
 CjeI  
 MseI  
 Hpy178III  
 BsrI  
 SfaNI  
 BpmI  
 MboII  
 MaeIII  
 601  
 CAAAGGAGCGTCTTTTCTTTTAACTGGCACTTCTGGAGATGCTCTTTTTAGTAACAACTC  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660  
 GTTTCCTCGCAGAAAGGAAAATTGACCGTGAAGACCTCTACGAGAAAAATCATTGTTGAG  
 MnlI  
 MunI  
 Tsp509I  
 MwoI  
 BseRI  
 SfcI  
 Cac8I  
 HaeII  
 HhaI  
 MwoI  
 661  
 TTATCAACAAAGGGAGGAGCAATTGCTACTACAGCAGGCGCTCGCATAGCAAATAACAC  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720  
 AAGTAGTTGTTTCCCTCCTCGTTAACGATGATGTCGTCGCGAGCGTATCGTTTTATTGTG  
 HgaI  
 BsaBI  
 HinfI  
 TfiI  
 Hpy178III  
 MaeII  
 MnlI  
 AccI  
 ClaI  
 TaqI  
 HaeII  
 HhaI  
 Hin4I  
 721  
 AGGTTATGTTAGATTCCCTATCTAACATAGCGTCTACGTGAGGAGGCGCTATCGATGATGA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780  
 TCCAATACAATCTAAGGATAGATTGTATCGCAGATGCAGTCCTCCGCGATAGCTACTACT  
 TaqI  
 MaeII  
 TaqI  
 ApoI  
 Tsp509I  
 BsmI  
 Fnu4HI  
 CviRI  
 TseI  
 CjePI  
 781  
 AGGCACGTCGATACTATCGAACAACAAATTTCTATATTTTGAAGGGAATGCAGCGAAAAC  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840  
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Fig. 2 (con't)

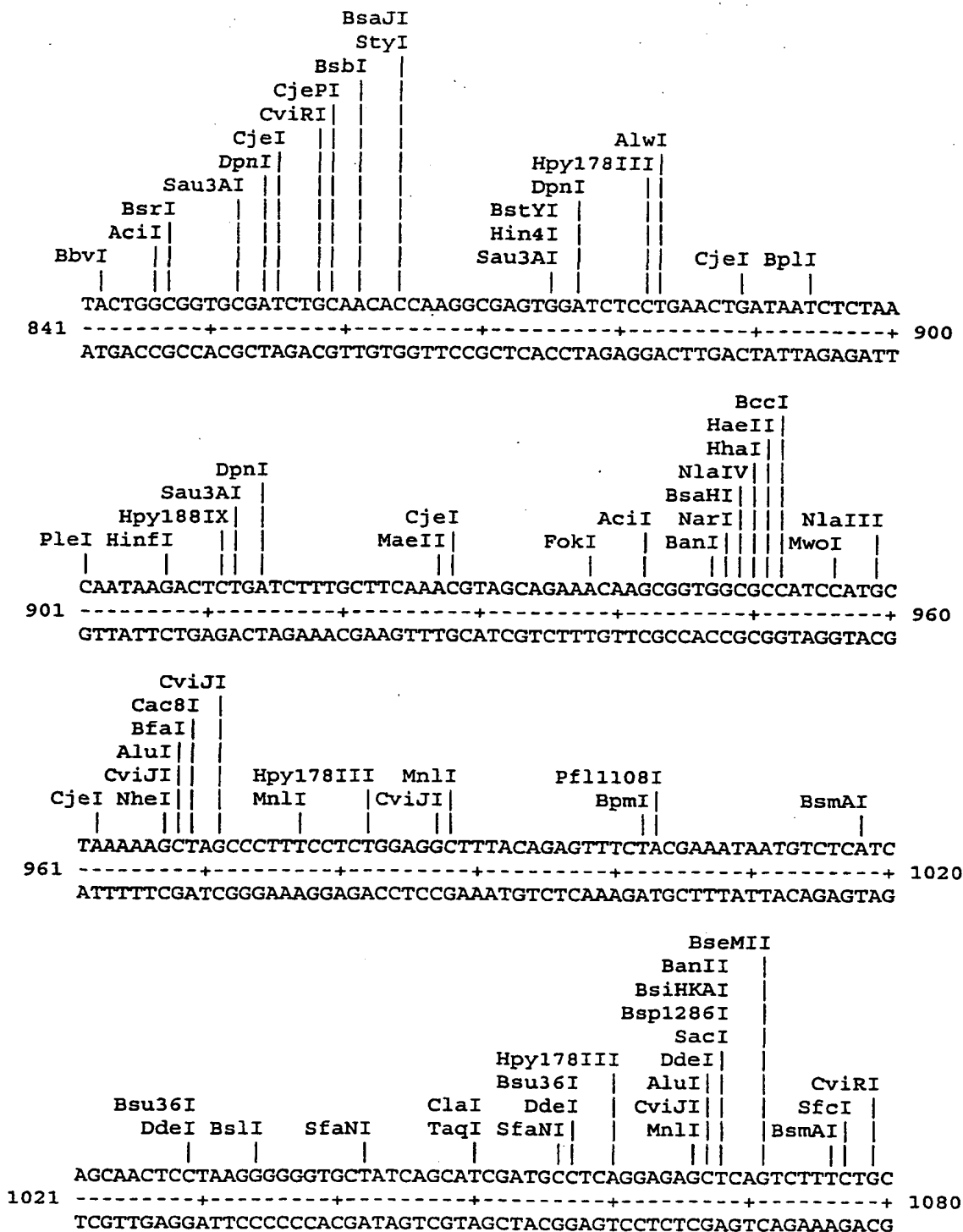
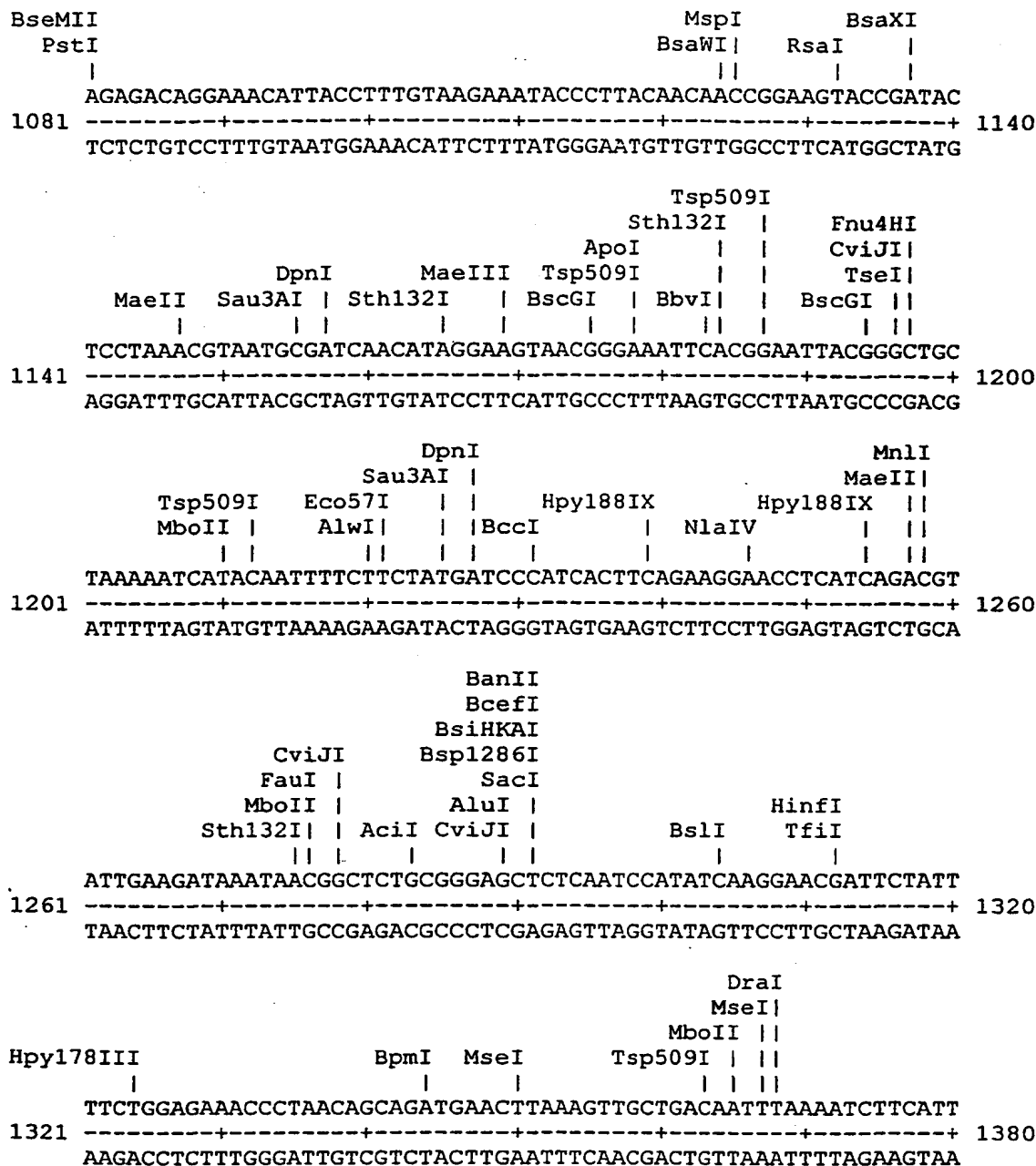


Fig. 2 (con't)



Hpy178III  
MspI  
BsaWI  
BsrI BspEI  
CviJI MnlI ||| MaeIII  
Fnu4HI || BbvI ||| Tsp45I Bce83I  
TseI || BsmAI ||| HinfI PleI |  
|| || ||| |||

CACGCAGCCAGTCTCCCTATCCGGAGGAAAGTTATTGCTACAAAAGGGAGTCACCTTTAGA  
1381 -----+-----+-----+-----+-----+-----+-----+ 1440  
GTGCGTCGGTCAGAGGGATAGGCCTCCTTTCAATAACGATGTTTTCCCTCAGTGAAATCT

MspI  
BseRI  
BsrFI  
CviJI  
HaeIII  
Hpy178III ||  
SmlI | ||  
MnlI | | ||  
Hin4I | | | ||  
AluI | | | | ||  
CviJI | | | | ||  
BsiHKAI | | | | ||  
Bsp1286I | | | | ||  
BssSI | | | | ||  
|| || || || ||

BsaJI NlaIII  
BplI BslI CjeI  
|| || || || ||

GAGCACGAGCTTCTCTCAAGAGGCCGGTTCTCTCCTCGGCATGGATTGAGGAACGACATT  
1441 -----+-----+-----+-----+-----+-----+ 1500  
CTCGTGCTCGAAGAGAGTTCTCCGGCCAAGAGAGGAGCCGTACCTAAGTCCTTGCTGTAA

HinfI  
AluI BfaI |  
CviJI AvrII | | Bsu36I  
MspAI BsaJI | | HinfI |  
PvuII CjeI || | HincII |  
SfcI | Hpy178III StyI TfiI PleI || DdeI  
| | || || ||

ATCAACTACAGCTGGGAGTATTACAATCACGAACCTAGGAATCAATGTTGACTCCTTAGG  
1501 -----+-----+-----+-----+-----+-----+ 1560  
TAGTTGATGTCGACCCTCATAATGTTAGTGCTTGGATCCTTAGTTACAACCTGAGGAATCC

BbvI  
CviJI  
Sth132I  
BscGI ||  
CviJI | ||  
Fnu4HI | | ||  
MseI | | | ||  
AflIII | | | ||  
SmlI TseI | | | ||  
|| || || || ||

BstAPI DpnI  
MwoI CjePI Sau3AI |  
|| || || || ||

TCTTAAGCAGCCCCGTGAGCCTAACAGCAAAGGTGCTTCAAATAAAGTGATCGTATCTGG  
1561 -----+-----+-----+-----+-----+-----+ 1620  
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AluI  
CviJI  
CjePI  
NdeI  
CviJI  
CjePI  
NlaIII  
MboII

GAAGCTCAACCTGATTGATATTGAAGGGAACATTTATGAAAGTCATATGTTTCAGCCATGA  
CTTCGAGTTGGACTAACTATAACTTCCCTTGTAATACTTTTCAGTATACAAGTCGGTACT

MseI  
AceIII  
TaaI  
AluI  
EarI  
SapI  
SfaNI  
CjePI  
BaeI  
HincII  
AclI  
MaeII

CCAGCTCTTCTCTCTATTAAAAATCACGGTTGATGCTGATGTTGATACTAACGTTGACAT  
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Hpy188IX  
AlwI  
Tsp509I  
DpnI  
NlaIV  
BamHI  
BstYI  
Sau3AI  
BbvCI  
Bpu10I  
BaeI  
CviJI  
Fnu4HI  
TseI  
MnlI  
BbvI  
BseMII  
DdeI  
AlwI  
BsaJI  
StyI  
HinfI  
TfiI

CAGCAGCCTTATCCCTGTTCTCTGCTGAGGATCCTAATTCAGAATACGGATTCCAAGGACA  
GTCGTGCGGAATAGGGACAAGGACGACTCCTAGGATTAAGTCTTATGCCTAAGGTTCTCTGT

BsaJI  
BstDSI  
CviJI  
HaeI  
AvaII  
Sau96I  
Tsp509I  
MseI  
BciVI  
AluI  
CviJI  
MnlI  
HaeIII

ATGGAATGTTAATTGGACTACGGATACAGCTACAAATACAAAGAGGCCACGGCAACTTG  
TACCTTACAATTAACCTGATGCCTATGTGCGATGTTTATGTTTTCTCCGGTGCCGTTGAAC

Bcefi  
CviJI  
Sth132I  
CviRI  
GACCAAAACAGGATTTGTTCCCGCCCCGAAAGAAAATCTGCGTTAGTATGCAATACCCT  
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Fig. 2 (con't)

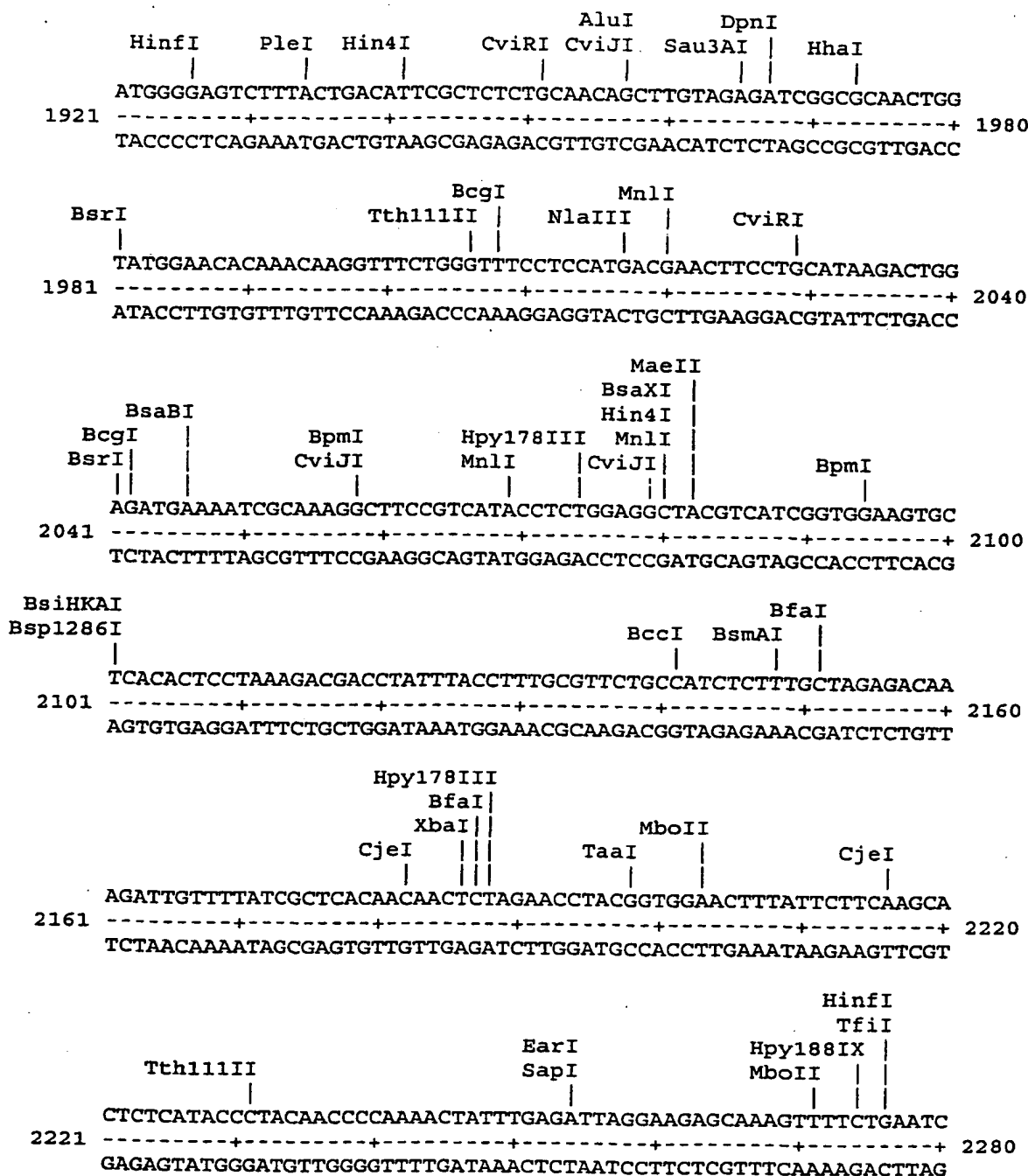
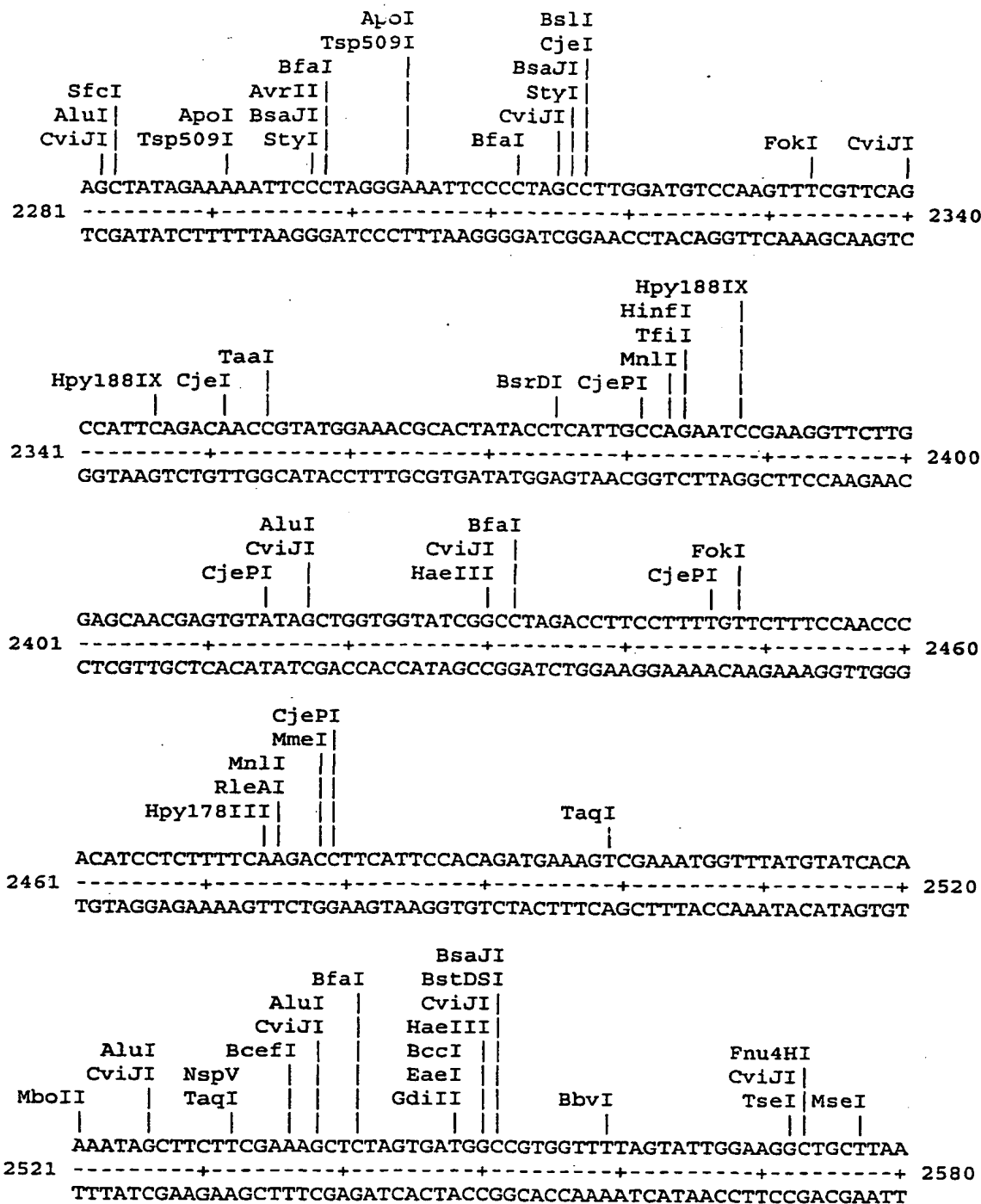


Fig. 2 (con't)



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Fig. 2 (con't)

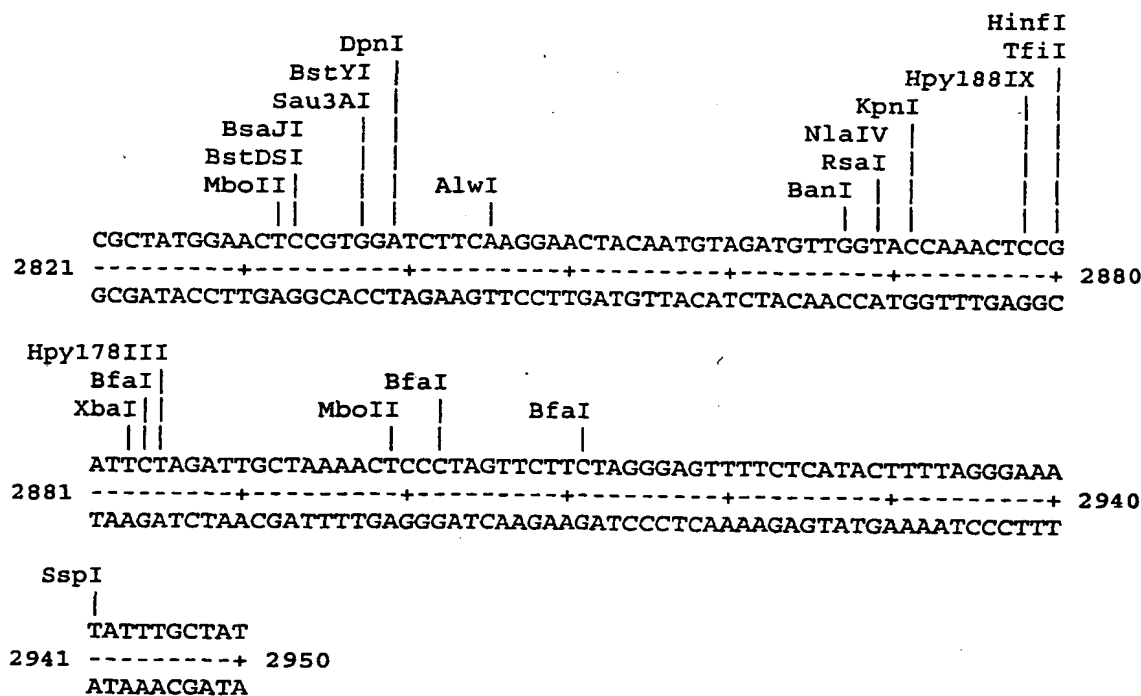




Figure 3: Nucleotide and deduced amino acid sequence of CPN100635

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agttaaagat gacaaaacag ctgtcaagaa tttttatctt gactctctga gttttctatt 60
ttatatgacg caagtaagaa ttttaataata aagtggggtt atg aaa tcg caa ttt 115
                                         Met Lys Ser Gln Phe
                                         1           5

tcc tgg tta gtg ctc tct tcg aca ttg gca tgt ttt act agt tgt tcc 163
Ser Trp Leu Val Leu Ser Ser Thr Leu Ala Cys Phe Thr Ser Cys Ser
                10                15                20

act gtt ttt gct gca act gct gaa aat ata ggc ccc tct gat agc ttt 211
Thr Val Phe Ala Ala Thr Ala Glu Asn Ile Gly Pro Ser Asp Ser Phe
                25                30                35

gac gga agt act aac aca ggc acc tat act cct aaa aat acg act act 259
Asp Gly Ser Thr Asn Thr Gly Thr Tyr Thr Pro Lys Asn Thr Thr Thr
                40                45                50

gga ata gac tat act ctg aca gga gat ata act ctg caa aac ctt ggg 307
Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr Leu Gln Asn Leu Gly
55                60                65

gat tcg gca gct tta acg aag ggt tgt ttt tct gac act acg gaa tct 355
Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser Asp Thr Thr Glu Ser
70                75                80                85

tta agc ttt gcc ggt aag ggg tac tca ctt tct ttt tta aat att aag 403
Leu Ser Phe Ala Gly Lys Gly Tyr Ser Leu Ser Phe Leu Asn Ile Lys
Leu Ser Phe Ala Gly Lys Gly Tyr Ser Leu Ser Phe Leu Asn Ile Lys
                90                95                100

tct agt gct gaa ggc gca gcc ctt tct gtt aca act gat aaa aat ctg 451
Ser Ser Ala Glu Gly Ala Ala Leu Ser Val Thr Thr Asp Lys Asn Leu
Ser Ser Ala Glu Gly Ala Ala Leu Ser Val Thr Thr Asp Lys Asn Leu
                105                110                115

tcg cta aca gga ttt tcg agt ctt act ttc tta gcg gcc cca tca tcg 499
Ser Leu Thr Gly Phe Ser Ser Leu Thr Phe Leu Ala Ala Pro Ser Ser
Ser Leu Thr Gly Phe Ser Ser Leu Thr Phe Leu Ala Ala Pro Ser Ser
                120                125                130

gta atc aca acc ccc tca gga aaa ggt gca gtt aaa tgt gga ggg gat 547
Val Ile Thr Thr Pro Ser Gly Lys Gly Ala Val Lys Cys Gly Gly Asp
Val Ile Thr Thr Pro Ser Gly Lys Gly Ala Val Lys Cys Gly Gly Asp
                135                140                145

ctt aca ttt gat aac aat gga act att tta ttt aaa caa gat tac tgt 595
Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe Lys Gln Asp Tyr Cys
Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe Lys Gln Asp Tyr Cys
150                155                160                165

```

Fig. 3 (con't)

gag gaa aat ggc gga gcc att tct acc aag aat ctt tct ttg aaa aac	643
Glu Glu Asn Gly Gly Ala Ile Ser Thr Lys Asn Leu Ser Leu Lys Asn	
Glu Glu Asn Gly Gly Ala Ile Ser Thr Lys Asn Leu Ser Leu Lys Asn	
170 175 180	
agc acg gga tcg att tct ttt gaa ggg aat aaa tcg agc gca aca ggg	691
Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys Ser Ser Ala Thr Gly	
Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys Ser Ser Ala Thr Gly	
185 190 195	
aaa aaa ggt ggg gct att tgt gct act ggt act gta gat att aca aat	739
Lys Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr Val Asp Ile Thr Asn	
Lys Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr Val Asp Ile Thr Asn	
200 205 210	
aat acg gct cct acc ctc ttc tcg aac aat att gct gaa gct gca ggt	787
Asn Thr Ala Pro Thr Leu Phe Ser Asn Asn Ile Ala Glu Ala Ala Gly	
Asn Thr Ala Pro Thr Leu Phe Ser Asn Asn Ile Ala Glu Ala Ala Gly	
215 220 225	
gga gct ata aat agc aca gga aac tgt aca att aca ggg aat acg tct	835
Gly Ala Ile Asn Ser Thr Gly Asn Cys Thr Ile Thr Gly Asn Thr Ser	
Gly Ala Ile Asn Ser Thr Gly Asn Cys Thr Ile Thr Gly Asn Thr Ser	
230 235 240 245	
ctt gta ttt tct gaa aat agt gtg aca gcg acc gca gga aat gga gga	883
Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr Ala Gly Asn Gly Gly	
Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr Ala Gly Asn Gly Gly	
250 255 260	
gct ctt tct gga gat gcc gat gtt acc ata tct ggg aat cag agt gta	931
Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser Gly Asn Gln Ser Val	
Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser Gly Asn Gln Ser Val	
265 270 275	
act ttc tca gga aac caa gct gta gct aat ggc gga gcc att tat gct	979
Thr Phe Ser Gly Asn Gln Ala Val Ala Asn Gly Gly Ala Ile Tyr Ala	
Thr Phe Ser Gly Asn Gln Ala Val Ala Asn Gly Gly Ala Ile Tyr Ala	
280 285 290	
aag aag ctt aca ctg gct tcc ggg ggg ggg ggg ggg aat ccc ttt tct	1027
Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly Gly Gly Asn Pro Phe Ser	
Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly Gly Gly Asn Pro Phe Ser	
295 300 305	
aac aat ata gtc caa ggt acc act gca ggt aat ggt gga gcc att tct	1075
Asn Asn Ile Val Gln Gly Thr Thr Ala Gly Asn Gly Gly Ala Ile Ser	
Asn Asn Ile Val Gln Gly Thr Thr Ala Gly Asn Gly Gly Ala Ile Ser	
310 315 320 325	
ata ctg gca gct gga gag tgt agt ctt ttc agc gaa gca ggg gac cat	1123
Ile Leu Ala Ala Gly Glu Cys Ser Leu Phe Ser Glu Ala Gly Asp His	
Ile Leu Ala Ala Gly Glu Cys Ser Leu Phe Ser Glu Ala Gly Asp His	
330 335 340	

Fig. 3 (con't)

tac ctt aat ggg aat gcc att gtt gca act aca cca caa act aca aaa	1171
Tyr Leu Asn Gly Asn Ala Ile Val Ala Thr Thr Pro Gln Thr Thr Lys	
Tyr Leu Asn Gly Asn Ala Ile Val Ala Thr Thr Pro Gln Thr Thr Lys	
345 350 355	
aga aat tct att gac ata gga tct act ggc aaa gat cac gaa tta cgt	1219
Arg Asn Ser Ile Asp Ile Gly Ser Thr Gly Lys Asp His Glu Leu Arg	
Arg Asn Ser Ile Asp Ile Gly Ser Thr Gly Lys Asp His Glu Leu Arg	
360 365 370	
gca ata tct ggg cat agc atc ttt ttc tac gat ccg att act gct aat	1267
Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp Pro Ile Thr Ala Asn	
Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp Pro Ile Thr Ala Asn	
375 380 385	
acg gct gcg gat tct aca gat act tta aat ctc aat aag gct gat gca	1315
Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu Asn Lys Ala Asp Ala	
Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu Asn Lys Ala Asp Ala	
390 395 400 405	
ggg aat agt aca gat tat agt ggg tcg att gtt ttt tct ggt gaa aag	1363
Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val Phe Ser Gly Glu Lys	
Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val Phe Ser Gly Glu Lys	
410 415 420	
ctc tct gaa gat gaa gca aaa gtt gca gac aac ctc act tct acg ctg	1411
Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn Leu Thr Ser Thr Leu	
Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn Leu Thr Ser Thr Leu	
425 430 435	
aag cag cct gta act cta act gca gga aat tta gta ctt aaa cgt ggt	1459
Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu Val Leu Lys Arg Gly	
Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu Val Leu Lys Arg Gly	
440 445 450	
gtc act ctc gat acg aaa ggc ttt act cag acc gcg ggt tcc tct gtt	1507
Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr Ala Gly Ser Ser Val	
Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr Ala Gly Ser Ser Val	
455 460 465	
att atg gat gcg ggc aca acg tta aaa gca agt aca gag gag gtc act	1555
Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser Thr Glu Glu Val Thr	
Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser Thr Glu Glu Val Thr	
470 475 480 485	
tta aca ggt ctt tcc att cct gta gac tct tta ggc gag ggt aag aaa	1603
Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu Gly Glu Gly Lys Lys	
Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu Gly Glu Gly Lys Lys	
490 495 500	
gtt gta att gct gct tct gca gca agt aaa aat gta gcc ctt agt ggt	1651
Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn Val Ala Leu Ser Gly	
Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn Val Ala Leu Ser Gly	
505 510 515	

Fig. 3 (con't)

ccg att ctt ctt ttg gat aac caa ggg aat gct tat gaa aat ccc gac	1699
Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala Tyr Glu Asn His Asp	
Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala Tyr Glu Asn His Asp	
520 525 530	
tta gga aaa act caa gac ttt tca ttt gtg cag ctc tct gct ctg ggt	1747
Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln Leu Ser Ala Leu Gly	
Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln Leu Ser Ala Leu Gly	
535 540 545	
act gca aca act aca gat gtt cca gcg gtt cct aca gta gca act cct	1795
Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro Thr Val Ala Thr Pro	
Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro Thr Val Ala Thr Pro	
550 555 560 565	
acg cac tat ggg tat caa ggt act tgg gga atg act tgg gtt gat gat	1843
Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met Thr Trp Val Asp Asp	
Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met Thr Trp Val Asp Asp	
570 575 580	
acc gca agc act cca aag act aag aca gcg aca tta gct tgg acc aat	1891
Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr Leu Ala Trp Thr Asn	
Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr Leu Ala Trp Thr Asn	
585 590 595	
aca ggc tac ctt ccg aat cct gag cgt caa gga cct tta gtt cct aat	1939
Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly Pro Leu Val Pro Asn	
Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly Pro Leu Val Pro Asn	
600 605 610	
agc ctt tgg gga tct ttt tca gac atc caa gcg att caa ggt gtc ata	1987
Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala Ile Gln Gly Val Ile	
Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala Ile Gln Gly Val Ile	
615 620 625	
gag aga agt gct ttg act ctt tgt tca gat cga ggc ttc tgg gct gcg	2035
Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg Gly Phe Trp Ala Ala	
Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg Gly Phe Trp Ala Ala	
630 635 640 645	
gga gtc gcc aat ttc tta gat aaa gat aag aaa ggg gaa aaa cgc aaa	2083
Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys Gly Glu Lys Arg Lys	
Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys Gly Glu Lys Arg Lys	
650 655 660	
tac cgt cat aaa tct ggt gga tat gct atc gga ggt gca gcg caa act	2131
Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly Gly Ala Ala Gln Thr	
Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly Gly Ala Ala Gln Thr	
665 670 675	
tgt tct gaa aac tta att agc ttt gcc ttt tgc caa ctc ttt ggt agc	2179
Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys Gln Leu Phe Gly Ser	
Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys Gln Leu Phe Gly Ser	
680 685 690	

Fig. 3 (con't)

gat aaa gat ttc tta gtc gct aaa aat cat act gat acc tat gca gga	2227
Asp Lys Asp Phe Leu Val Ala Lys Asn His Thr Asp Thr Tyr Ala Gly	
Asp Lys Asp Phe Leu Val Ala Lys Asn His Thr Asp Thr Tyr Ala Gly	
695 700 705	
gcc ttc tat atc caa cac att aca gaa tgt agt ggg ttc ata ggt tgt	2275
Ala Phe Tyr Ile Gln His Ile Thr Glu Cys Ser Gly Phe Ile Gly Cys	
Ala Phe Tyr Ile Gln His Ile Thr Glu Cys Ser Gly Phe Ile Gly Cys	
710 715 720 725	
ctc tta gat aaa ctt cct ggc tct tgg agt cat aaa ccc ctc gtt tta	2323
Leu Leu Asp Lys Leu Pro Gly Ser Trp Ser His Lys Pro Leu Val Leu	
Leu Leu Asp Lys Leu Pro Gly Ser Trp Ser His Lys Pro Leu Val Leu	
730 735 740	
gaa ggg cag ctc gct tat agc cac gtc agt aat gat ctg aag aca aag	2371
Glu Gly Gln Leu Ala Tyr Ser His Val Ser Asn Asp Leu Lys Thr Lys	
Glu Gly Gln Leu Ala Tyr Ser His Val Ser Asn Asp Leu Lys Thr Lys	
745 750 755	
tat act gcg tat cct gag gtg aaa ggt tct tgg ggg aat aat gct ttt	2419
Tyr Thr Ala Tyr Pro Glu Val Lys Gly Ser Trp Gly Asn Asn Ala Phe	
Tyr Thr Ala Tyr Pro Glu Val Lys Gly Ser Trp Gly Asn Asn Ala Phe	
760 765 770	
aac atg atg ttg gga gct tct tct cat tct tat cct gaa tac ctg cat	2467
Asn Met Met Leu Gly Ala Ser Ser His Ser Tyr Pro Glu Tyr Leu His	
Asn Met Met Leu Gly Ala Ser Ser His Ser Tyr Pro Glu Tyr Leu His	
775 780 785	
tgt ttt gat acc tat gct cca tac atc aaa ctg aat ctg acc tat ata	2515
Cys Phe Asp Thr Tyr Ala Pro Tyr Ile Lys Leu Asn Leu Thr Tyr Ile	
Cys Phe Asp Thr Tyr Ala Pro Tyr Ile Lys Leu Asn Leu Thr Tyr Ile	
790 795 800 805	
cgt cag gac agc ttc tcg gag aaa ggt aca gaa gga aga tct ttt gat	2563
Arg Gln Asp Ser Phe Ser Glu Lys Gly Thr Glu Gly Arg Ser Phe Asp	
Arg Gln Asp Ser Phe Ser Glu Lys Gly Thr Glu Gly Arg Ser Phe Asp	
810 815 820	
gac agc aac ctc ttc aat tta tct ttg cct ata ggg gtg aag ttt gag	2611
Asp Ser Asn Leu Phe Asn Leu Ser Leu Pro Ile Gly Val Lys Phe Glu	
Asp Ser Asn Leu Phe Asn Leu Ser Leu Pro Ile Gly Val Lys Phe Glu	
825 830 835	
aag ttc tct gat tgt aat gac ttt tct tat gat ctg act tta tcc tat	2659
Lys Phe Ser Asp Cys Asn Asp Phe Ser Tyr Asp Leu Thr Leu Ser Tyr	
Lys Phe Ser Asp Cys Asn Asp Phe Ser Tyr Asp Leu Thr Leu Ser Tyr	
840 845 850	
gtt cct gat ctt atc cgc aat gat ccc aaa tgc act aca gca ctt gta	2707
Val Pro Asp Leu Ile Arg Asn Asp Pro Lys Cys Thr Thr Ala Leu Val	
Val Pro Asp Leu Ile Arg Asn Asp Pro Lys Cys Thr Thr Ala Leu Val	
855 860 865	

Fig. 3 (con't)

atc agc gga gcc tct tgg gaa act tat gcc aat aac tta gca cga cag 2755  
Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn Asn Leu Ala Arg Gln  
Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn Asn Leu Ala Arg Gln  
870 875 880 885

gcc ttg caa gtg cgt gca ggc agt cac tac gcc ttc tct cct atg ttt 2803  
Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala Phe Ser Pro Met Phe  
Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala Phe Ser Pro Met Phe  
890 895 900

gaa gtg ctc ggc cag ttt gtc ttt gaa gtt cgt gga tcc tca cgg att 2851  
Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg Gly Ser Ser Arg Ile  
Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg Gly Ser Ser Arg Ile  
905 910 915

tat aat gta gat ctt ggg ggt aag ttc caa ttc taggagcgtc tctcatgtct 2904  
Tyr Asn Val Asp Leu Gly Gly Lys Phe Gln Phe  
Tyr Asn Val Asp Leu Gly Gly Lys Phe Gln Phe  
920 925

cagaaattct gagagagatc gcatttagga ttttcttaaa cacgac 2950

Figure 4: Restriction enzyme analysis of CPN100635

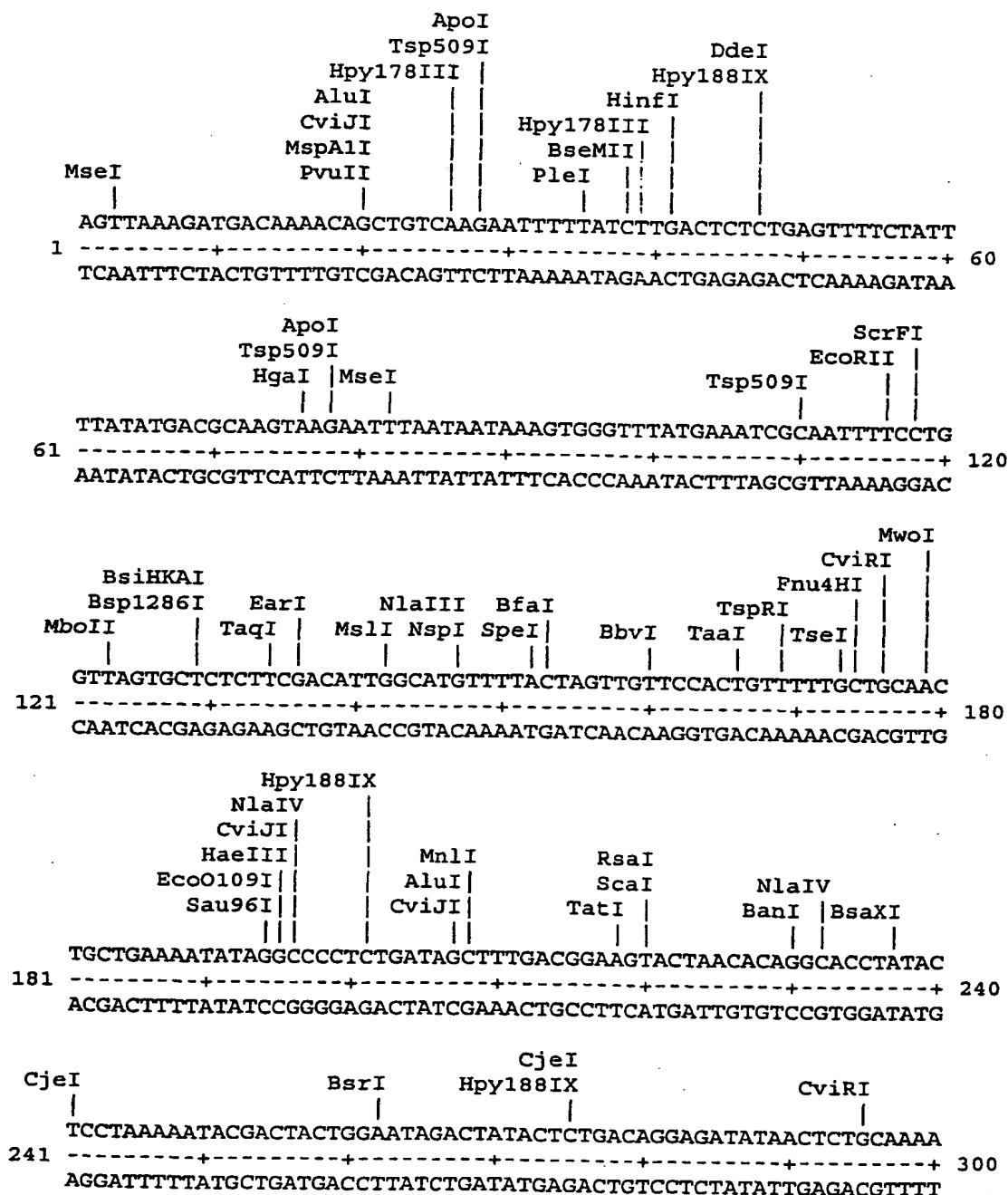


Fig. 4 (con't)

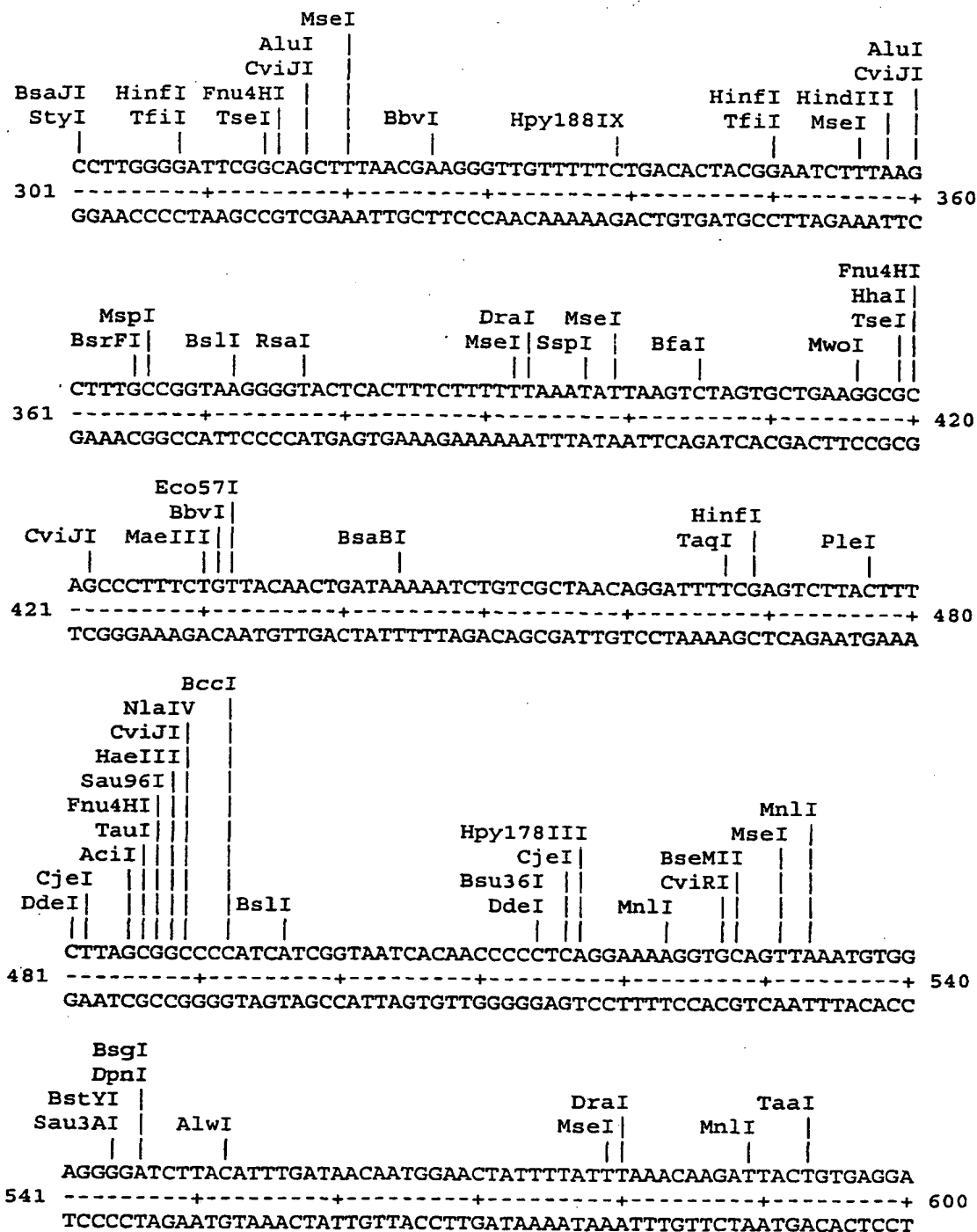
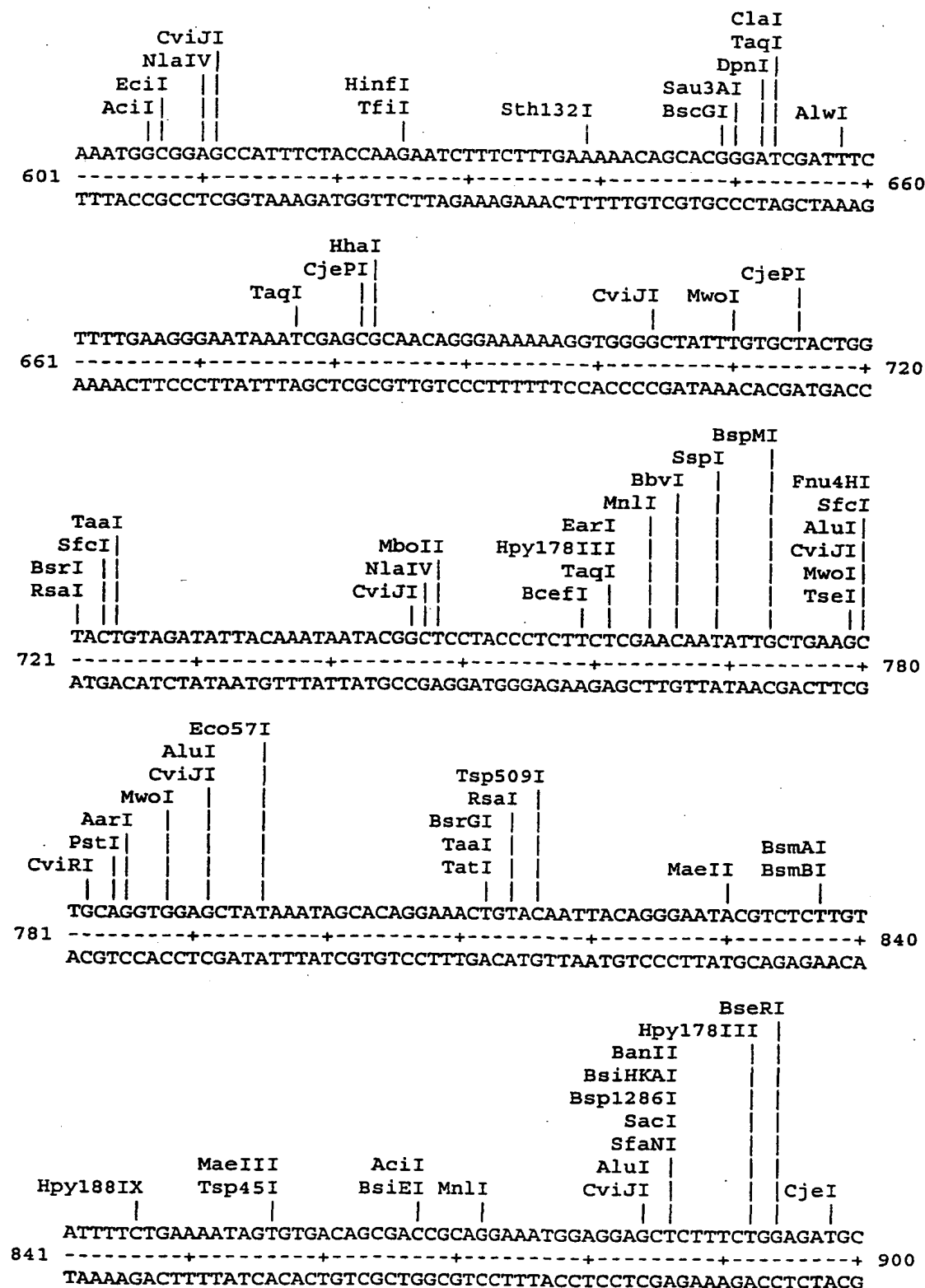




Fig. 4 (con't)



**SUBSTITUTE SHEET (RULE 26)**

AluI  
CviJI  
MspAII  
PvuII  
BsrI  
Fnu4HI  
TseI  
BbvI  
BpmI  
NlaIV  
AvaII  
Sau96I  
BsmFI  
MseI  
XcmI  
DpnI  
BstYI  
Sau3AI  
HaeIV  
Hin4I  
BcgI  
AlwI  
ApoI  
Tsp509I  
CviRI  
MwoI  
BsmI  
CATTGTGTGCAACTACACCACAACTACAAAAAGAAATTCTATTGACATAGGATCTACTGG  
GTAACAACGTTGATGTGGTGTGTTTCTTTAAGATAACTGTATCCTAGATGACC  
CAAAGATCACGAATTACGTGCAATATCTGGGCATAGCATCTTTTTCTACGATCCGATTAC  
GTTTCTAGTGCTTAATGCACGTTATAGACCCGTATCGTAGAAAAAGATGCTAGGCTAATG  
TGCTAATACGGCTGCGGATTCTACAGATACTTTAAATCTCAATAAGGCTGATGCAGGTAA  
ACGATTATGCCGACGCCCTAAGATGTCTATGAAATTTAGAGTTATTCCGACTACGTCCATT  
TAGTACAGATTATAGTGGGTCGATTGTTTTTCTGGTGAAAAGCTCTCTGAAGATGAAGC  
ATCATGTCTAATATCACCCAGCTAACAAAAAAGACCCTTTTCGAGAGACTTCTACTTTCG

Fig. 4 (con't)

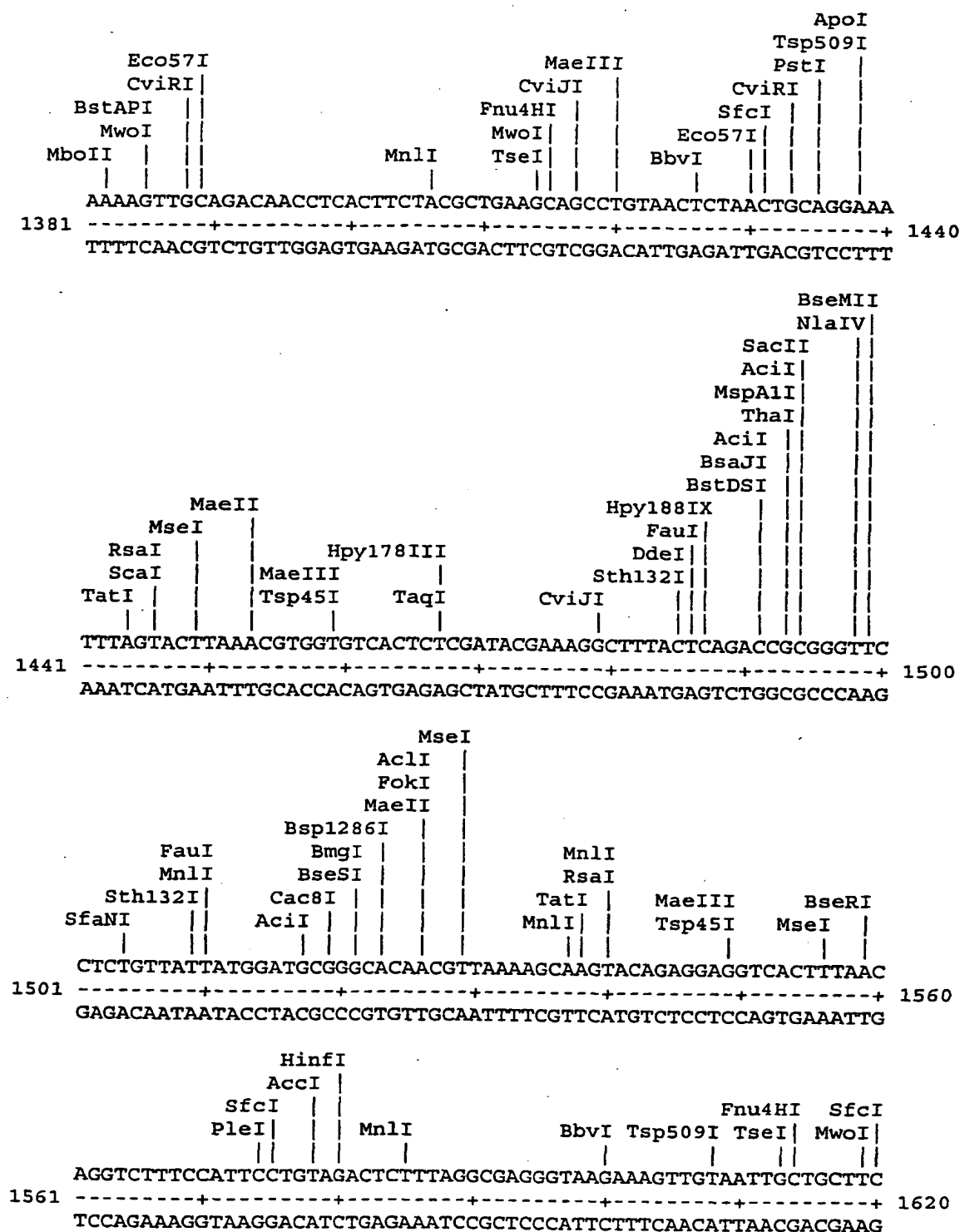
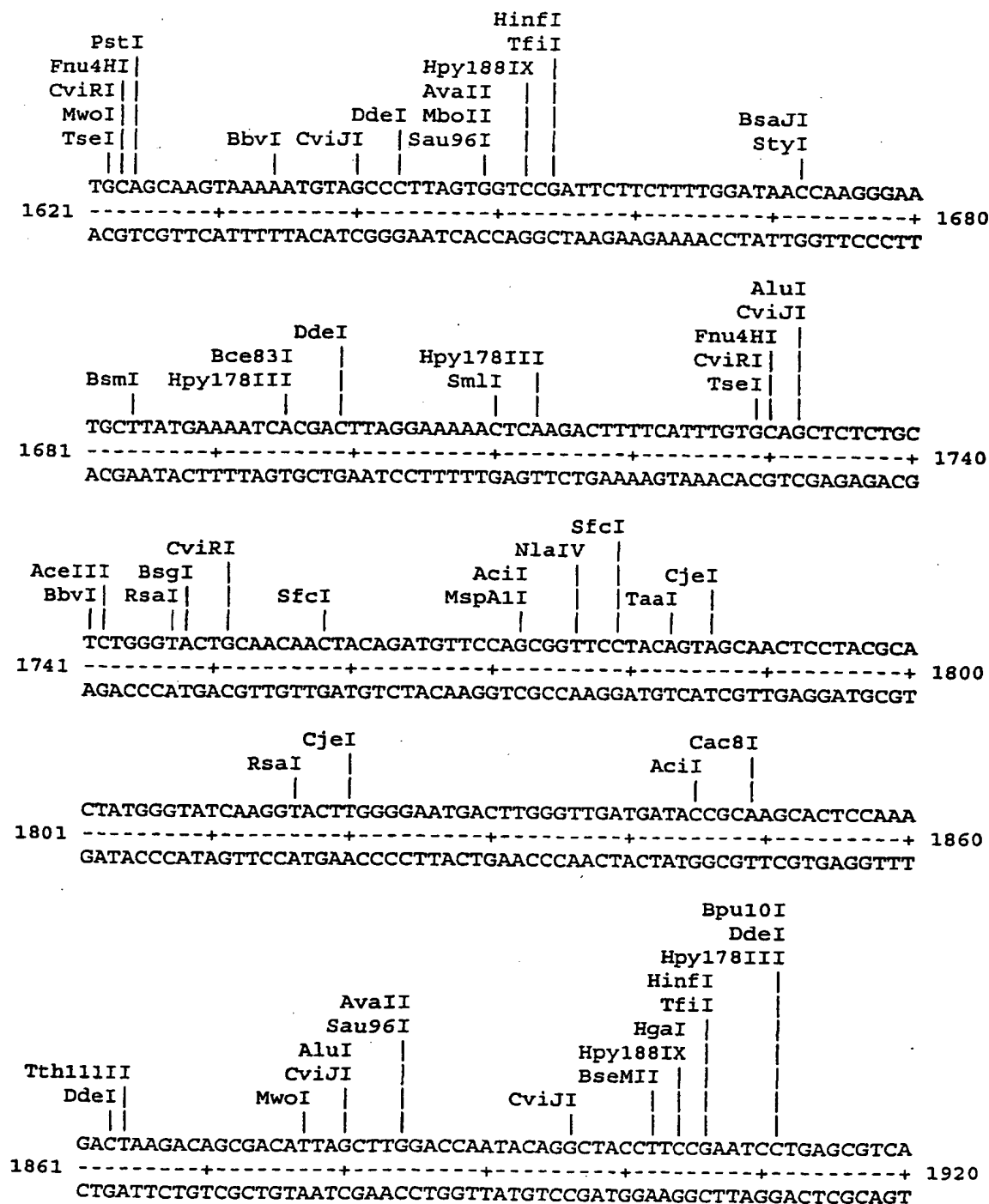


Fig. 4 (con't)



IvaII  
 EcoO109I  
 Psp5II  
 Sau96I  
 Sse8647I  
 A10I  
 CviJI  
 DpnI  
 BstYI  
 FokI  
 Sau3AI  
 Hpy188IX  
 AlwI  
 HinfI  
 TfiI  
 1921  
 AGGACCTTTAGTTCCTAATAGCCTTTGGGGATCTTTTTTCAGACATCCAAGCGATTCAAGG  
 TCCTGGAAATCAAGGATTATCGGAAACCCCTAGAAAAAGTCTGTAGGTTTCGCTAAGTTCC  
 1980  
 MwoI  
 HinfI  
 BbvI  
 TaqI  
 DpnI  
 Sau3AI  
 Hpy188IX  
 MnlI  
 PleI  
 HinfI  
 Sth132I  
 CviJI  
 TseI  
 Fnu4HI  
 CviJI  
 FauI  
 2040  
 TGTCATAGAGAGAAGTGCTTTGACTCTTTGTTCAGATCGAGGCTTCTGGGCTGCGGGAGT  
 ACAGTATCTCTCTTCACGAAACTGAGAAACAAGTCTAGCTCCGAAGACCCGACGCCCTCA  
 2041  
 PleI  
 Tsp509I  
 DdeI  
 TaaI  
 2100  
 CGCCAATTTCTTAGATAAAAGATAAGAAAGGGGAAAAACGCAATACCGTCATAAATCTGG  
 GCGGTAAAGAATCTATTCTATTCTTTCCCTTTTTCGCTTATGGCAGTATTTAGACC  
 2101  
 Hpy188IX  
 MnlI  
 HaeIV  
 Hin4I  
 Fnu4HI  
 CviRI  
 TseI  
 HhaI  
 Hpy188IX  
 BbvI  
 BsgI  
 MseI  
 Tsp509I  
 AluI  
 CviJI  
 2160  
 TGGATATGCTATCGGAGGTGCAGCGCAAACCTTGTTCTGAAAACCTTAATTAGCTTTGCCTT  
 ACCTATACGATAGCCTCCACGTCGCGTTTGAACAAGACTTTTGAATTAATCGAAACGGAA  
 2161  
 BstXI  
 DdeI  
 2220  
 TTGCCAACTCTTTGGTAGCGATAAAGATTCTTAGTCGCTAAAAATCATACTGATACCTA  
 AACGGTTGAGAAACCATCGCTATTCTTAAAGAATCAGCGATTTTTAGTATGACTATGGAT  
 2221  
 CviJI  
 NlaIV  
 CviRI  
 BsbI  
 MmeI  
 BsmAI  
 DdeI  
 2280  
 TGCAGGAGCCTTCTATATCCAACACATTACAGAATGTAGTGGGTTTCATAGGTTGTCTCTT  
 ACGTCTCGGAAGATATAGGTTGTGTAATGTCTTACATCACCCAAGTATCCAACAGAGAA

Fig. 4 (con't)

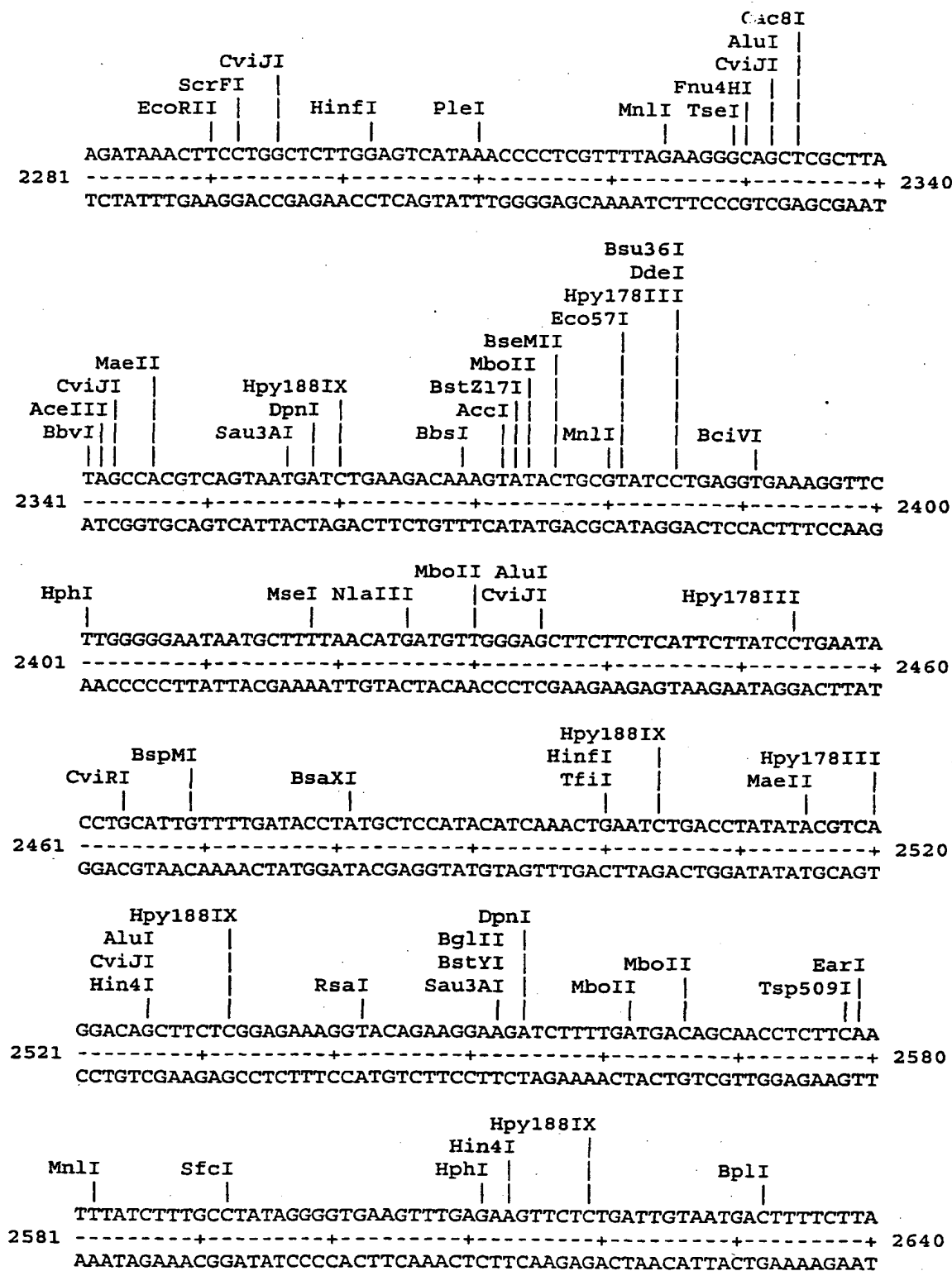


Fig. 4 (con't)

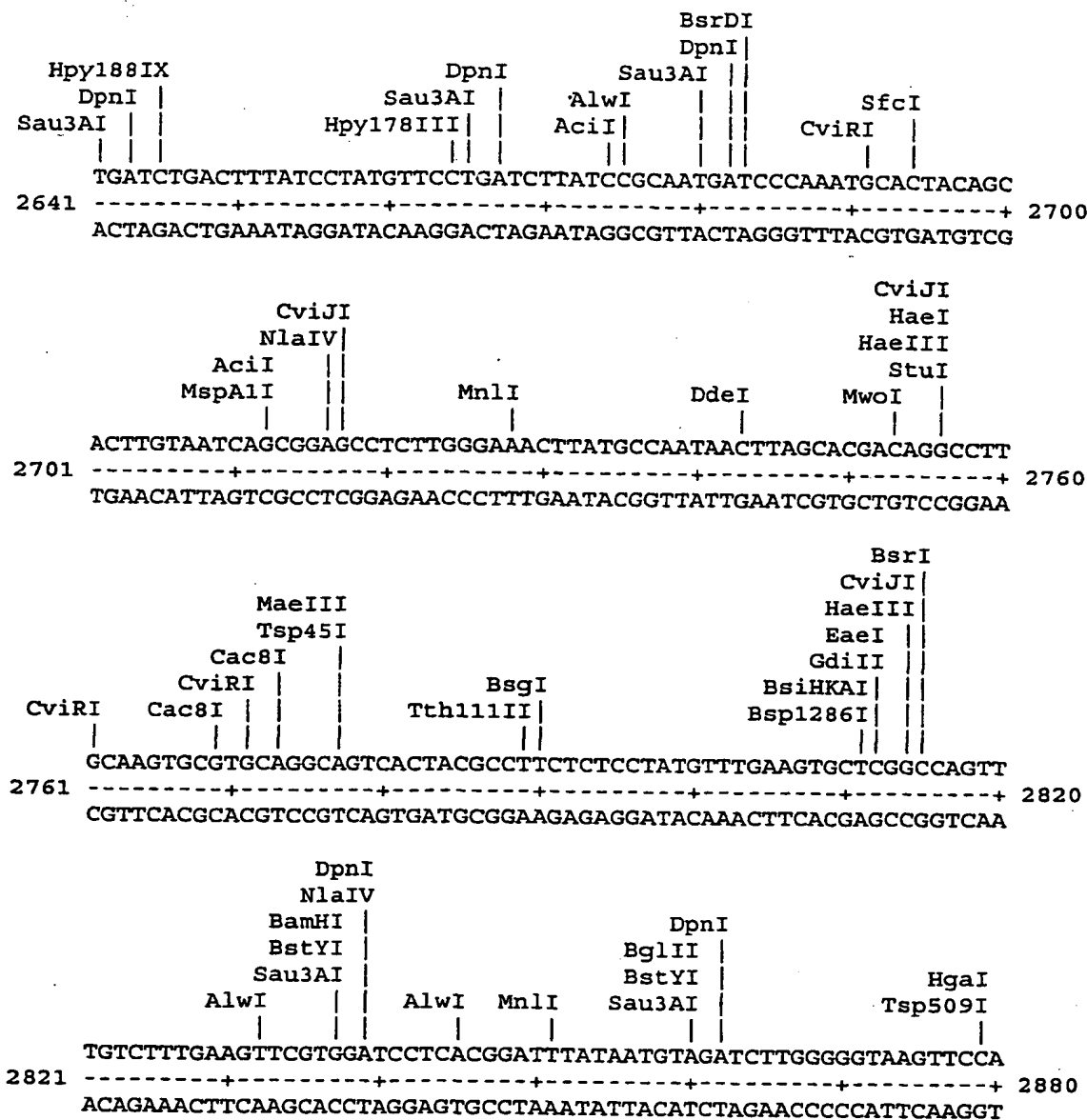




Fig. 4 (con't)

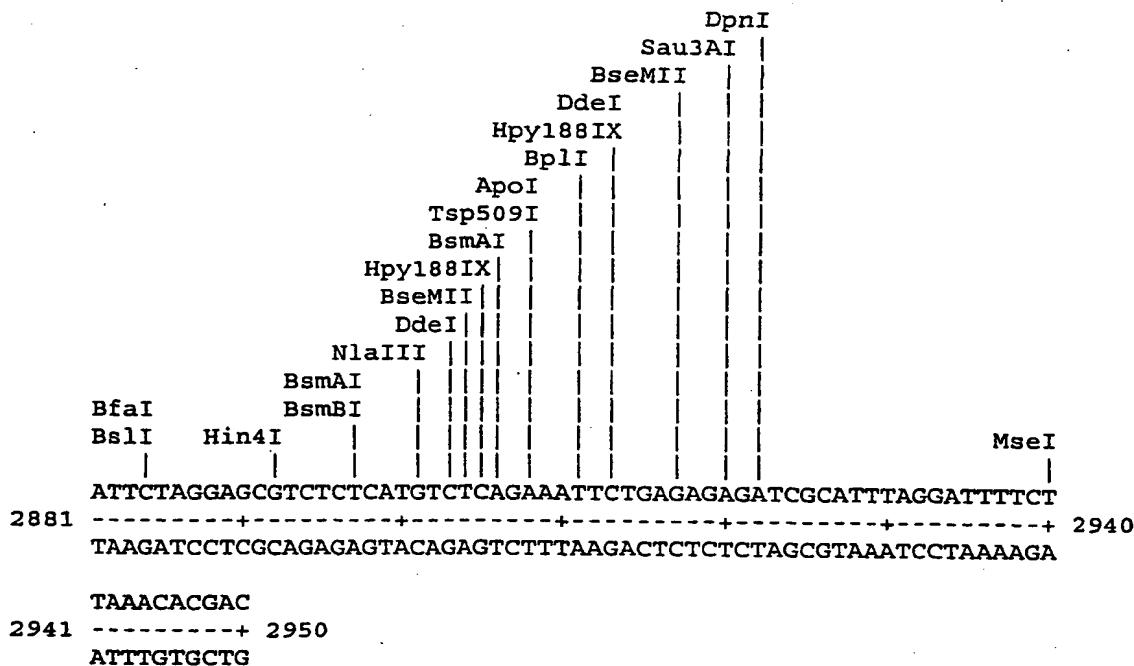


Figure 5: Nucleotide and deduced amino acid sequence of CPN100638

```

tgtagattct taacttacta gtctctcctt tctctttgct ttctttaatt tattgcagta 60
tgtggtgaaa taatttggtta aaccacctat agccctctac atg aaa tcc tct ctt 115
                                         Met Lys Ser Ser Leu
                                         1           5
cat tgg ttt tta atc tcg tca tct tta gca ctt ccc ttg tca cta aat 163
His Trp Phe Leu Ile Ser Ser Ser Leu Ala Leu Pro Leu Ser Leu Asn
          10           15           20
ttc tct gcg ttt gct gct gtt gtt gaa atc aat cta gga cct acc aat 211
Phe Ser Ala Phe Ala Ala Val Val Glu Ile Asn Leu Gly Pro Thr Asn
          25           30           35
agc ttc tct gga cca gga acc tac act cct cca gcc caa aca aca aat 259
Ser Phe Ser Gly Pro Gly Thr Tyr Thr Pro Pro Ala Gln Thr Thr Asn
          40           45           50
gca gat gga act atc tat aat cta aca ggg gat gtc tca atc acc aat 307
Ala Asp Gly Thr Ile Tyr Asn Leu Thr Gly Asp Val Ser Ile Thr Asn
          55           60           65
gca gga tct ccg aca gct cta acc gct tcc tgc ttt aaa gaa act act 355
Ala Gly Ser Pro Thr Ala Leu Thr Ala Ser Cys Phe Lys Glu Thr Thr
          70           75           80           85
ggg aat ctt tct ttc caa ggc cac ggc tac caa ttt ctc cta caa aat 403
Gly Asn Leu Ser Phe Gln Gly His Gly Tyr Gln Phe Leu Leu Gln Asn
          90           95           100
atc gat gcg gga gcg aac tgt acc ttt acc aat aca gct gca aat aag 451
Ile Asp Ala Gly Ala Asn Cys Thr Phe Thr Asn Thr Ala Ala Asn Lys
          105           110           115
ctt ctc tcc ttt tca gga ttc tcc tat ttg tca cta ata caa acc acg 499
Leu Leu Ser Phe Ser Gly Phe Ser Tyr Leu Ser Leu Ile Gln Thr Thr
          120           125           130
aat gct acc aca gga aca gga gcc atc aag tcc aca gga gct tgt tct 547
Asn Ala Thr Thr Gly Thr Gly Ala Ile Lys Ser Thr Gly Ala Cys Ser
          135           140           145
att cag tcg aac tat agt tgc tac ttt ggc caa aac ttt tct aat gac 595
Ile Gln Ser Asn Tyr Ser Cys Tyr Phe Gly Gln Asn Phe Ser Asn Asp
          150           155           160           165
aat gga ggc gcc ctc caa ggc agc tct atc agt cta tcg cta aac ccc 643
Asn Gly Gly Ala Leu Gln Gly Ser Ser Ile Ser Leu Ser Leu Asn Pro
          170           175           180
aac cta acg ttt gcc aaa aac aaa gca acg caa aaa ggg ggt gcc ctc 691
Asn Leu Thr Phe Ala Lys Asn Lys Ala Thr Gln Lys Gly Gly Ala Leu
          185           190           195

```

Fig. 5 (con't)

tat tcc acg gga ggg act aca att aac aat acg tta aac tca gca tca	739
Tyr Ser Thr Gly Gly Ile Thr Ile Asn Asn Thr Leu Asn Ser Ala Ser	
200 205 210	
ttt tct gaa aat acc gcg gcg aac aat ggc gga gcc att tac acg gaa	787
Phe Ser Glu Asn Thr Ala Ala Asn Asn Gly Gly Ala Ile Tyr Thr Glu	
215 220 225	
gct agc agt ttt att agc agc aac aaa gca att agc ttt ata aac aat	835
Ala Ser Ser Phe Ile Ser Ser Asn Lys Ala Ile Ser Phe Ile Asn Asn	
230 235 240 245	
agt gtg acc gca acc tca gct aca ggg gga gcc att tac tgt agt agt	883
Ser Val Thr Ala Thr Ser Ala Thr Gly Gly Ala Ile Tyr Cys Ser Ser	
250 255 260	
aca tca gcc ccc aaa cca gtc tta act cta tca gac aac ggg gaa ctg	931
Thr Ser Ala Pro Lys Pro Val Leu Thr Leu Ser Asp Asn Gly Glu Leu	
265 270 275	
aac ttt ata gga aat aca gca att act agt ggt ggg gcg att tat act	979
Asn Phe Ile Gly Asn Thr Ala Ile Thr Ser Gly Gly Ala Ile Tyr Thr	
280 285 290	
gac aat cta gtt ctt tct tct gga gga cct acg ctt ttt aaa aac aac	1027
Asp Asn Leu Val Leu Ser Ser Gly Gly Pro Thr Leu Phe Lys Asn Asn	
295 300 305	
tct ggc tat gat act gca gct ccc tta gga gga gca att gcg att gct	1075
Ser Gly Tyr Asp Thr Ala Ala Pro Leu Gly Gly Ala Ile Ala Ile Ala	
310 315 320 325	
gac tct gga tct ttg agt ctt tcg gct ctt ggt gga gac atc act ttt	1123
Asp Ser Gly Ser Leu Ser Leu Ser Ala Leu Gly Gly Asp Ile Thr Phe	
330 335 340	
gaa gga aac aca gta gtc aaa gga gct tct tcg agt cag acc act acc	1171
Glu Gly Asn Thr Val Val Lys Gly Ala Ser Ser Ser Gln Thr Thr Thr	
345 350 355	
aga aat tct att aac atc gga aac acc aat gct aag att gta cag ctg	1219
Arg Asn Ser Ile Asn Ile Gly Asn Thr Asn Ala Lys Ile Val Gln Leu	
360 365 370	
cga gcc tct caa ggc aat act atc tac ttc tat gat cct ata aca act	1267
Arg Ala Ser Gln Gly Asn Thr Ile Tyr Phe Tyr Asp Pro Ile Thr Thr	
375 380 385	
agc atc act gca gct ctc tca gat gct cta aac tta aat ggt cct gac	1315
Ser Ile Thr Ala Ala Leu Ser Asp Ala Leu Asn Leu Asn Gly Pro Asp	
390 395 400 405	
ctt gca ggg aat cct gca tat caa gga acc atc gta ttt tct gga gag	1365
Leu Ala Gly Asn Pro Ala Tyr Gln Gly Thr Ile Val Phe Ser Gly Glu	
410 415 420	

Fig. 5 (con't)

aag ctc tcg gaa gca gaa gct gca gaa gct gat aat ctc aaa tct aca	1411
Lys Leu Ser Glu Ala Glu Ala Ala Glu Ala Asp Asn Leu Lys Ser Thr	
425 430 435	
att cag caa cct cta act ctt gcg gga ggg caa ctc tct ctt aaa tca	1459
Ile Gln Gln Pro Leu Thr Leu Ala Gly Gly Gln Leu Ser Leu Lys Ser	
440 445 450	
gga gtc act cta gtt gct aag tcc ttt tcg caa tct ccg ggc tct acc	1507
Gly Val Thr Leu Val Ala Lys Ser Phe Ser Gln Ser Pro Gly Ser Thr	
455 460 465	
ctc ctc atg gat gca ggg acc aca tta gaa acc gct gat ggg atc act	1555
Leu Leu Met Asp Ala Gly Thr Thr Leu Glu Thr Ala Asp Gly Ile Thr	
470 475 480 485	
atc aat aat ctt gtt ctc aat gta gat tcc tta aaa gag acc aag aag	1603
Ile Asn Asn Leu Val Leu Asn Val Asp Ser Leu Lys Glu Thr Lys Lys	
490 495 500	
ggc acg cta aaa gca aca caa gca agt cag aca gtc act tta tct gga	1651
Gly Thr Leu Lys Ala Thr Gln Ala Ser Gln Thr Val Thr Leu Ser Gly	
505 510 515	
tcg ctc tct ctt gta gat cct tct gga aat gtc tac gaa gat gtc tct	1699
Ser Leu Ser Leu Val Asp Pro Ser Gly Asn Val Tyr Glu Asp Val Ser	
520 525 530	
tgg aat aac cct caa gtc ttt tct tgt ctc act ctt act gct gac gac	1747
Trp Asn Asn Pro Gln Val Phe Ser Cys Leu Thr Leu Thr Ala Asp Asp	
535 540 545	
ccc gcg aat att cac atc aca gac tta gct gct gat ccc cta gaa aaa	1795
Pro Ala Asn Ile His Ile Thr Asp Leu Ala Ala Asp Pro Leu Glu Lys	
550 555 560 565	
aat cct atc cat tgg gga tac caa ggg aat tgg gca tta tct tgg caa	1843
Asn Pro Ile His Trp Gly Tyr Gln Gly Asn Trp Ala Leu Ser Trp Gln	
570 575 580	
gag gat act gcg act aaa tcc aaa gca gcg act ctt acc tgg aca aaa	1891
Glu Asp Thr Ala Thr Lys Ser Lys Ala Ala Thr Leu Thr Trp Thr Lys	
585 590 595	
aca gga tac aat ccg aat cct gag cgt cgt gga acc tta gtt gct aac	1939
Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Gly Thr Leu Val Ala Asn	
600 605 610	
acg cta tgg gga tcc ttt gtt gat gtg cgc tcc ata caa cag ctt gta	1987
Thr Leu Trp Gly Ser Phe Val Asp Val Arg Ser Ile Gln Gln Leu Val	
615 620 625	
gcc act aaa gta cgc caa tct caa gaa act cgc ggc atc tgg tqt gaa	2035
Ala Thr Lys Val Arg Gln Ser Gln Glu Thr Arg Gly Ile Trp Cys Glu	
630 635 640 645	

Fig. 5 (con't)

ggg atc tcg aac ttc ttc cat aaa gat agc acg aag ata aat aaa ggt	2083
Gly Ile Ser Asn Phe Phe His Lys Asp Ser Thr Lys Ile Asn Lys Gly	
650 655 660	
ttt cgc cac ata agt gca ggt tat gtt gta gga gcg act aca aca tta	2131
Phe Arg His Ile Ser Ala Gly Tyr Val Val Gly Ala Thr Thr Thr Leu	
665 670 675	
gct tct gat aat ctt atc act gca gcc ttc tgc caa tta ttc ggg aaa	2179
Ala Ser Asp Asn Leu Ile Thr Ala Ala Phe Cys Gln Leu Phe Gly Lys	
680 685 690	
gat aga gat cac ttt ata aat aaa aat aga gct tct gcc tat gca gct	2227
Asp Arg Asp His Phe Ile Asn Lys Asn Arg Ala Ser Ala Tyr Ala Ala	
695 700 705	
tct ctc cat ctc cag cat cta gcg acc ttg tct tct cca agc ttg tta	2275
Ser Leu His Leu Gln His Leu Ala Thr Leu Ser Ser Pro Ser Leu Leu	
710 715 720 725	
cgc tac ctt cct gga tct gaa agt gag cag cct gtc ctc ttt gat gct	2323
Arg Tyr Leu Pro Gly Ser Glu Ser Glu Gln Pro Val Leu Phe Asp Ala	
730 735 740	
cag atc agc tat atc tat agt aaa aat act atg aaa acc tat tac acc	2371
Gln Ile Ser Tyr Ile Tyr Ser Lys Asn Thr Met Lys Thr Tyr Tyr Thr	
745 750 755	
caa gca cca aag gga gag agc tcg tgg tat aat gac ggt tgc gct ctg	2419
Gln Ala Pro Lys Gly Glu Ser Ser Trp Tyr Asn Asp Gly Cys Ala Leu	
760 765 770	
gaa ctt gcg agc tcc cta cca cac act gct tta agc cat gag ggt ctc	2467
Glu Leu Ala Ser Ser Leu Pro His Thr Ala Leu Ser His Glu Gly Leu	
775 780 785	
ttc cac gcg tat ttt cct ttc atc aaa gta gaa gct tcg tac ata cac	2515
Phe His Ala Tyr Phe Pro Phe Ile Lys Val Glu Ala Ser Tyr Ile His	
790 795 800 805	
caa gat agc ttc aaa gaa cgt aat act acc ttg gta cga tct ttc gat	2563
Gln Asp Ser Phe Lys Glu Arg Asn Thr Thr Leu Val Arg Ser Phe Asp	
810 815 820	
agc ggt gat tta att aac gtc tct gtg cct att gga att acc ttc gag	2611
Ser Gly Asp Leu Ile Asn Val Ser Val Pro Ile Gly Ile Thr Phe Glu	
825 830 835	
aga ttc tcg aga aac gag cgt gcg tct tac gaa gct act gtc atc tac	2659
Arg Phe Ser Arg Asn Glu Arg Ala Ser Tyr Glu Ala Thr Val Ile Tyr	
840 845 850	
gtt gcc gat gtc tat cgt aag aat cct gac tgc acg aca gct ctc cta	2707
Val Ala Asp Val Tyr Arg Lys Asn Pro Asp Cys Thr Thr Ala Leu Leu	
855 860 865	

Fig. 5 (con't)

atc aac aat acc tcg tgg aaa act aca gga acg aat ctc tca aga caa	2755
Ile Asn Asn Thr Ser Trp Lys Thr Thr Gly Thr Asn Leu Ser Arg Gln	
870 875 880 885	
gct ggt atc gga aga gca ggg atc ttt tat gcc ttc tct cca aat ctt	2803
Ala Gly Ile Gly Arg Ala Gly Ile Phe Tyr Ala Phe Ser Pro Asn Leu	
890 895 900	
gag gtc aca agt aac cta tct atg gaa att cgt gga tct tca cgc agc	2851
Glu Val Thr Ser Asn Leu Ser Met Glu Ile Arg Gly Ser Ser Arg Ser	
905 910 915	
tac aat gca gat ctt gga ggt aag ttc cag ttc taaaagcggt cctgatccct	2904
Tyr Asn Ala Asp Leu Gly Gly Lys Phe Gln Phe	
920 925	
tagaaattct aagagatcct gagtgatatct agggacttct caaaga	2950

Figure 6: Restriction enzyme analysis of CPN100638

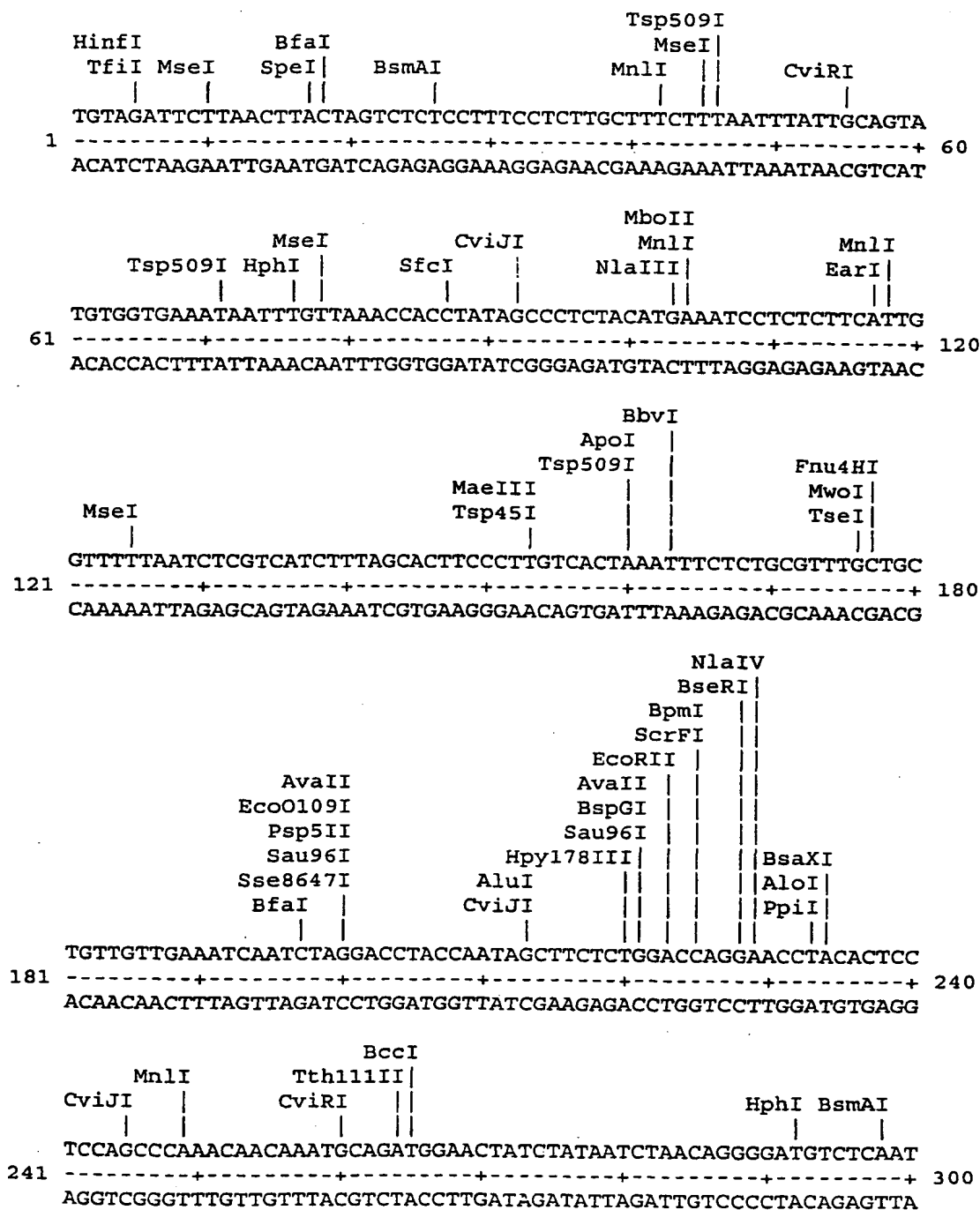


Fig. 6 (con't)

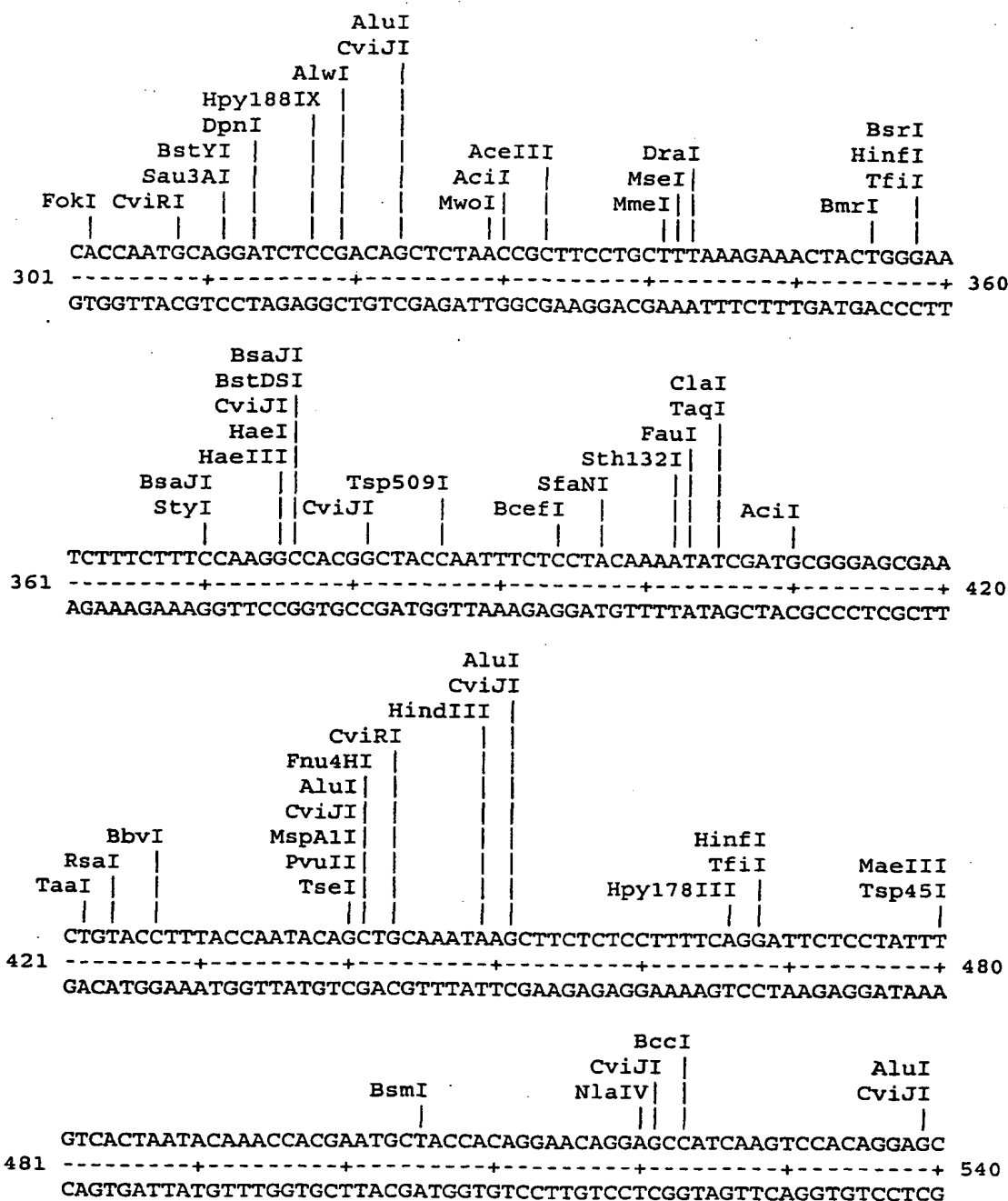




Fig. 6 (con't)

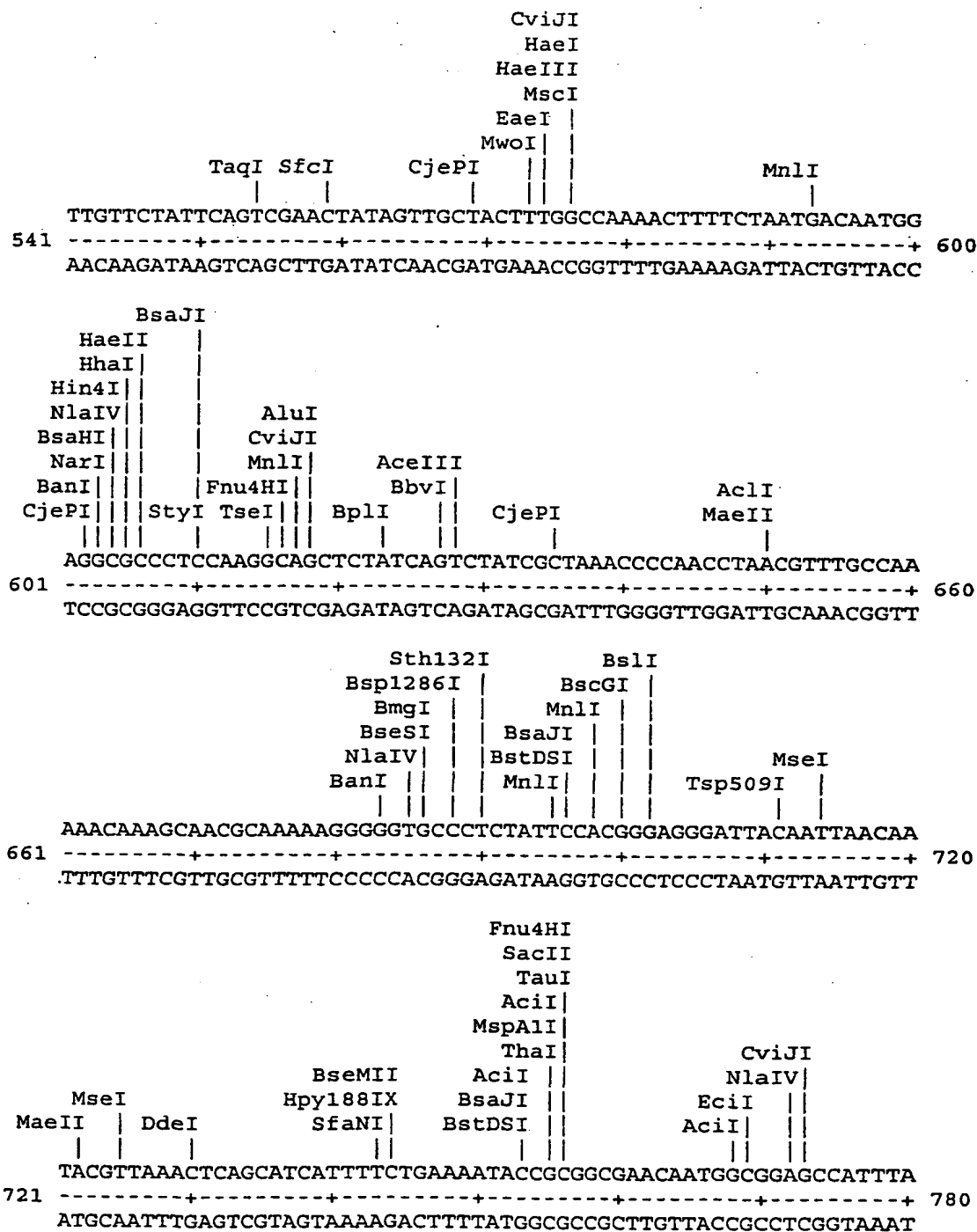


Fig. 6 (con't)

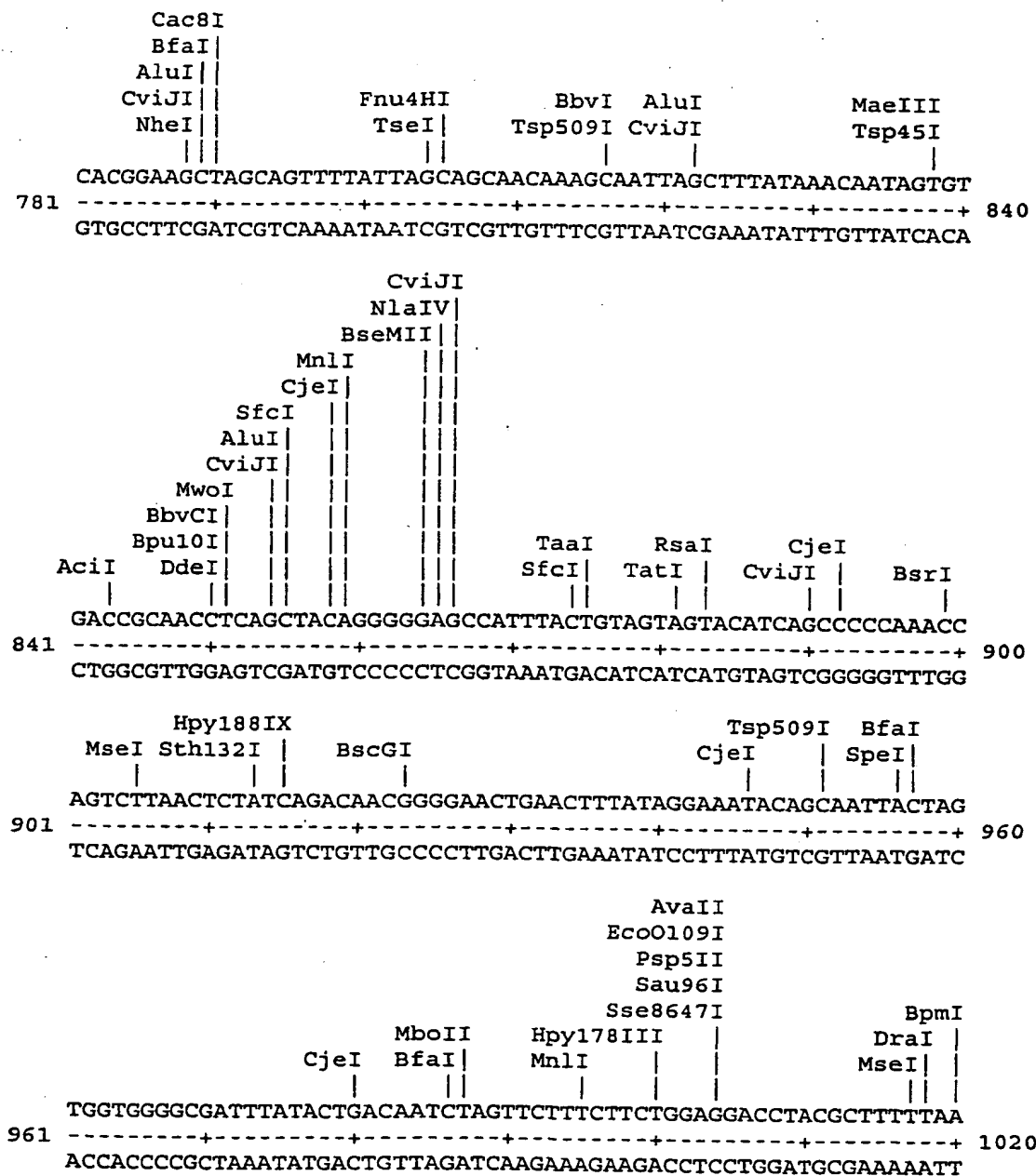


Fig. 6 (con't)

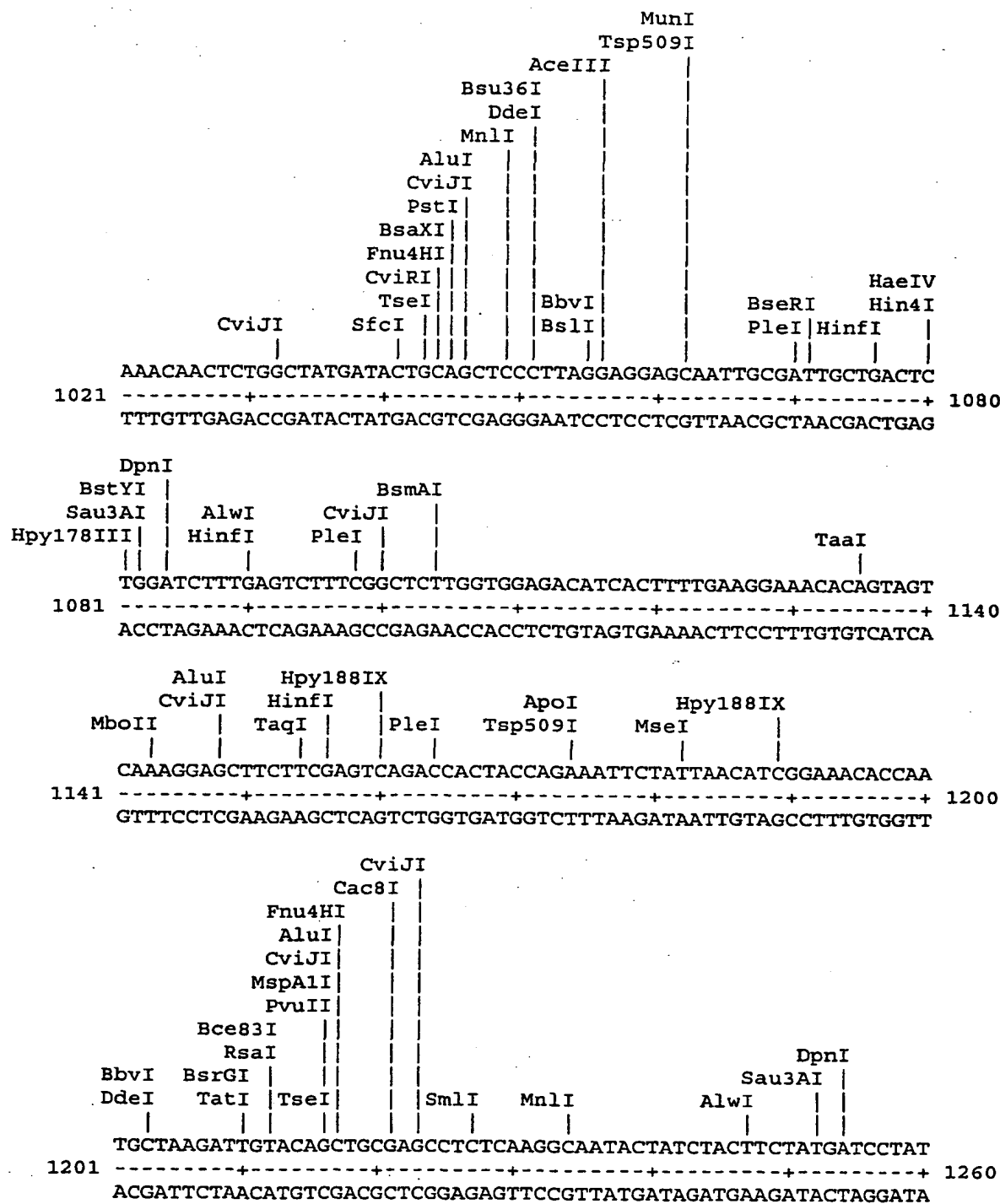


Fig. 6 (con't)

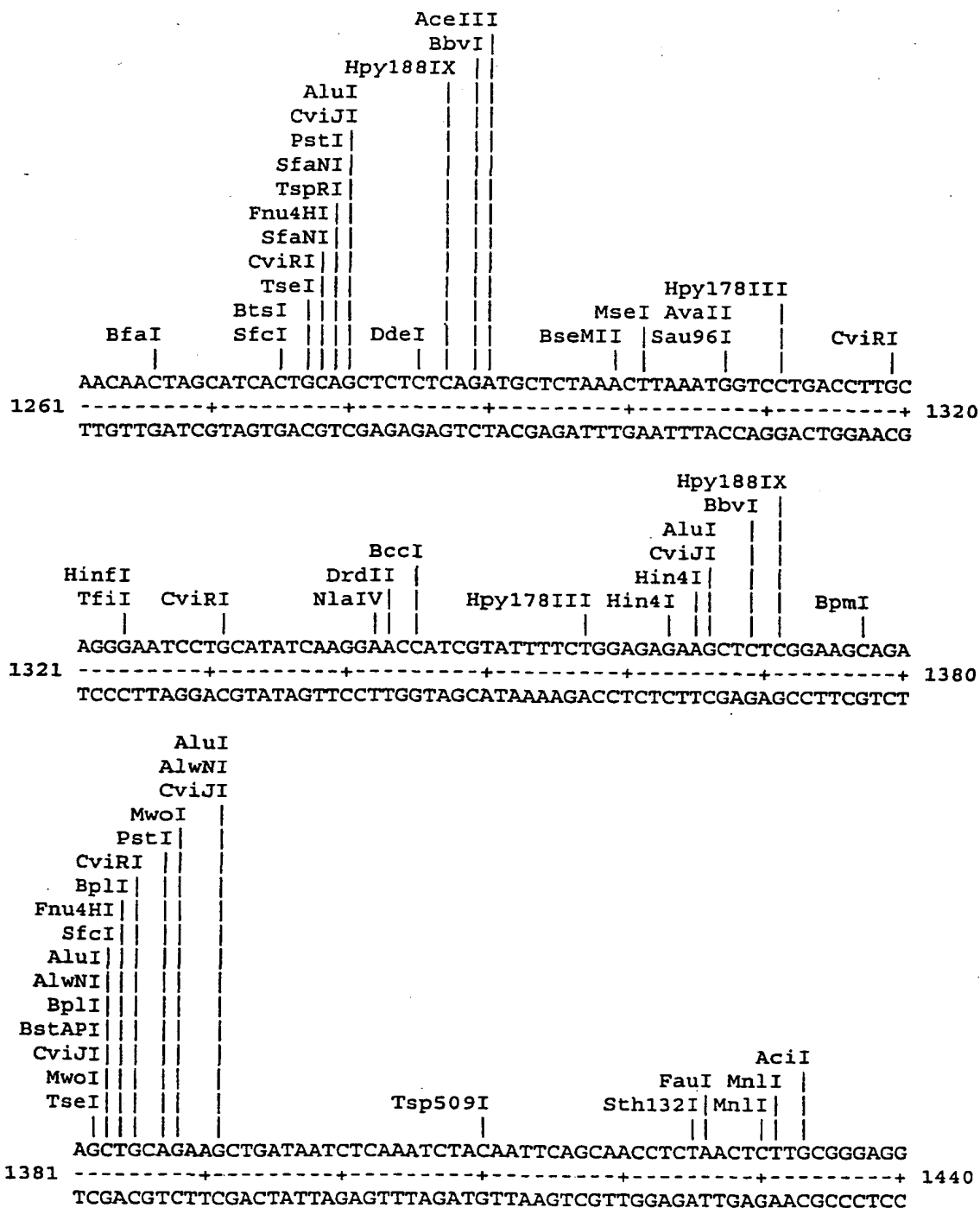


Fig. 6 (con't)

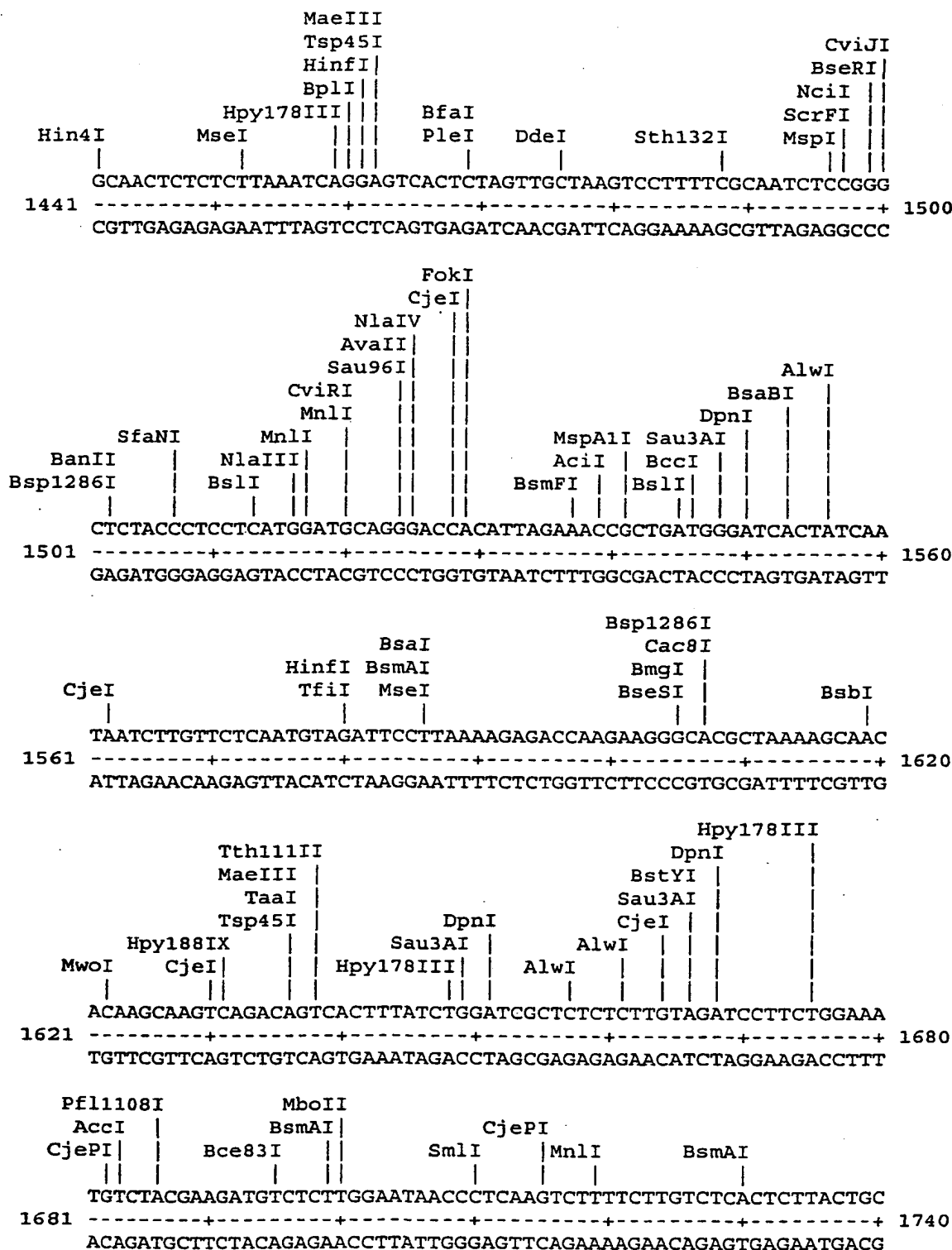
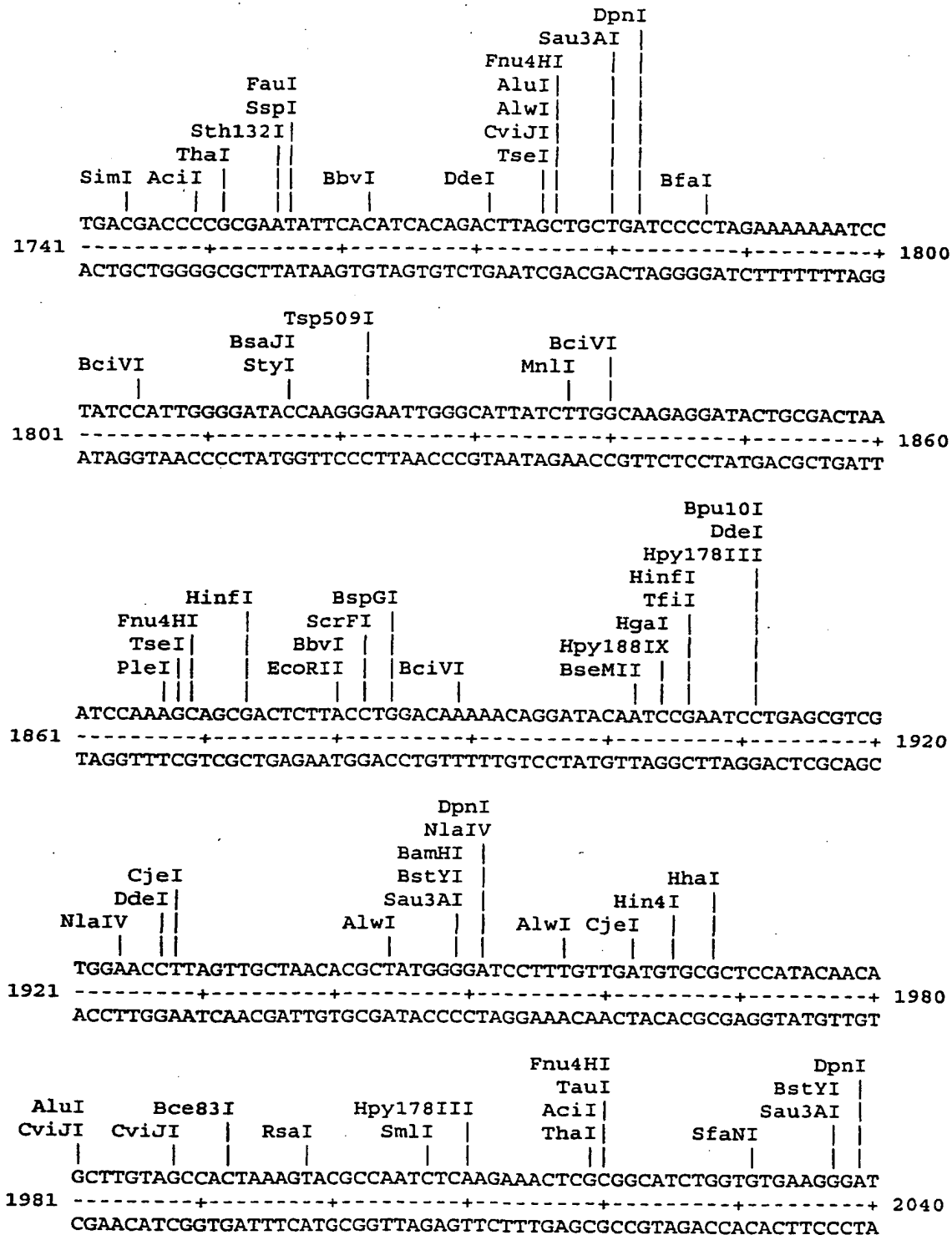
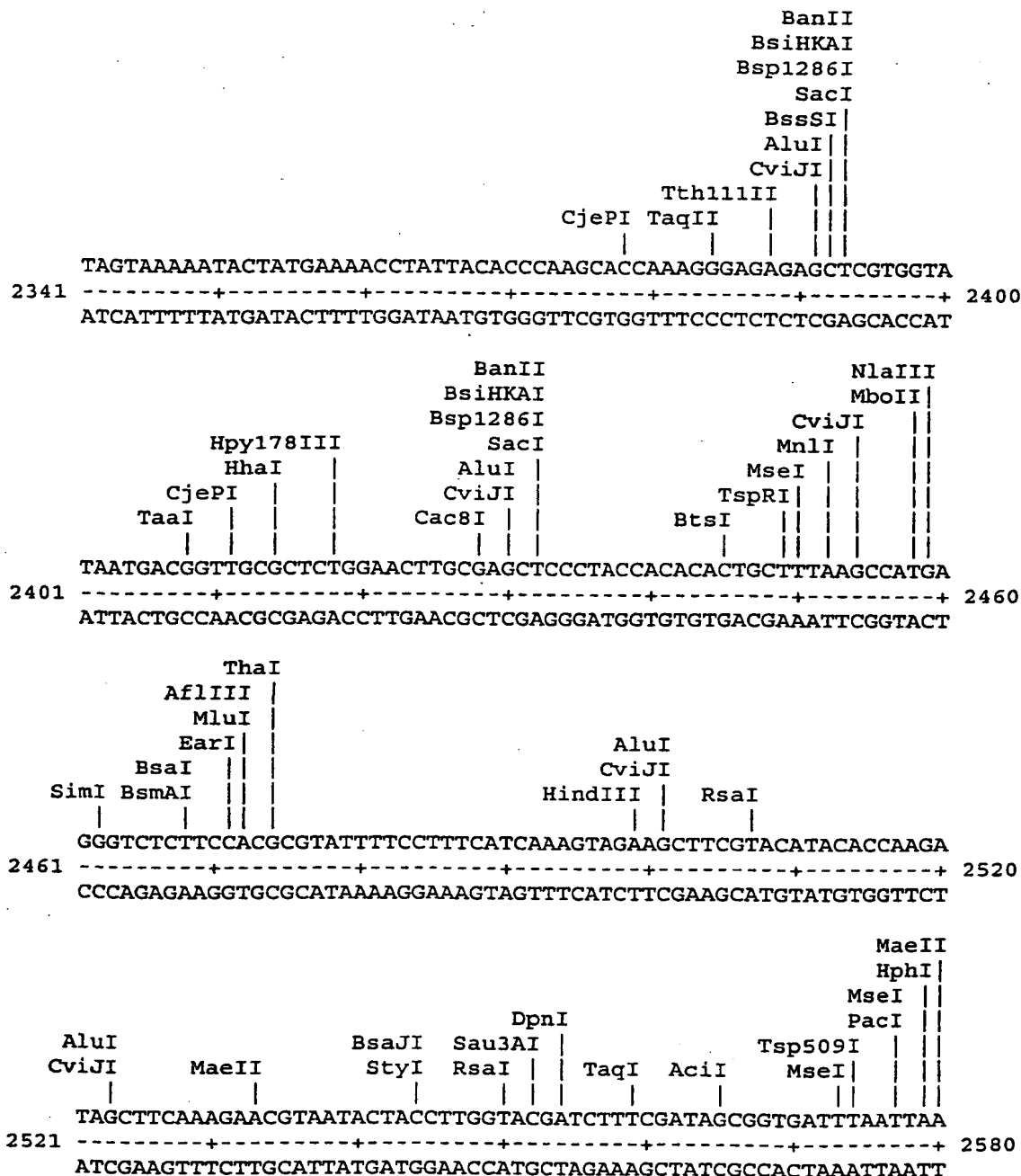


Fig. 6 (con't)



XmnI  
 AlwI  
 Hpy178III  
 TaqI  
 MboII  
 MboII  
 BspMI  
 MslI  
 CviRI  
 2041  
 CTCGAACCTTCTTCCATAAAGATAGCACGAAGATAAAAGGTTTTTCGCCACATAAGTGC  
 GAGCTTGAAGAAGGTATTTCTATCGTGCTTCTATTTATTTCCAAAAGCGGTGTATTTCAGC  
 2100  
 CviJI  
 PstI  
 TspRI  
 Fnu4HI  
 CviRI  
 TseI  
 BtsI  
 SfiI  
 Hpy188IX  
 AluI  
 CviJI  
 BsgI  
 2101  
 AGGTTATGTTGTAGGAGCGACTACAACATTAGCTTCTGATAATCTTATCACTGCAGCCTT  
 TCCAATACAACATCCTCGCTGATGTTGTAATCGAAGACTATTAGAATAGTGACGTCGGAA  
 2160  
 BbvI  
 Tsp509I  
 Sth132I  
 Hpy178III  
 Sau3AI  
 BsaBI  
 DpnI  
 AluI  
 CviJI  
 2161  
 CTGCCAATTATTTCGGGAAAGATAGAGATCACTTTATAAATAAAAATAGAGCTTCTGCCTA  
 GACGGTTAATAAGCCCTTTCTATCTCTAGTGAAATATTTATTTTATCTCGAAGACGGAT  
 2220  
 AluI  
 CviJI  
 Fnu4HI  
 BpmI  
 CviRI  
 MwoI  
 TseI  
 BbvI  
 BccI  
 BfaI  
 Tth111I  
 SfaNI  
 BbsI  
 MboII  
 MaeIII  
 AluI  
 CviJI  
 HindIII  
 MwoI  
 2221  
 TGCAGCTTCTCTCCATCTCCAGCATCTAGCGACCTTGTCTTCTCCAAGCTTGTTACGCTA  
 ACGTCGAAGAGAGGTAGAGGTCGTAGATCGCTGGAACAGAAGAGGTTCTGAACAATGCGAT  
 2280  
 SfiI  
 BseMII  
 AluI  
 CviJI  
 DpnI  
 Hpy188IX  
 BstYI  
 Sau3AI  
 ScrFI  
 EcoRII  
 AlwI  
 TseI  
 BbvI  
 SfaNI  
 CviJI  
 Fnu4HI  
 MnlI  
 2281  
 CCTTCCTGGATCTGAAAGTGAGCAGCCTGTCTCTTTGATGCTCAGATCAGCTATATCTA  
 GGAAGGACCTAGACTTTCACTCGTCGGACAGGAGAACTACGAGTCTAGTCGATATAGAT  
 2340

Fig. 6 (con't)





HpaI  
 Hpy178III  
 Hpy178III  
 TaqI  
 AvaI  
 SmlI  
 Hin4I  
 HinfI  
 BsmAI  
 BsmBI  
 Tsp509I  
 Hpy178III  
 TaqI  
 TfiI  
 XhoI  
 BplI  
 Cac8I  
 Hin4I  
 CGTCTCTGTGCCTATTGGAATTACCTTCGAGAGATTCTCGAGAAACGAGCGTGCCTCTTA  
 2581 -----+-----+-----+-----+-----+ 2640  
 GCAGAGACACGGATAACCTTAATGGAAGCTCTCTAAGAGCTCTTTGCTCGCACGCAGAAT  
 Hpy178III  
 AluI  
 CviJI  
 TaaI  
 MaeII  
 BsaBI  
 BsgI  
 HinfI  
 TfiI  
 CviRI  
 CviJI  
 CGAAGCTACTGTCTATCTACGTTGCCGATGTCTATCGTAAGAATCCTGACTGCACGACAGC  
 2641 -----+-----+-----+-----+-----+ 2700  
 GCTTCGATGACAGTAGATGCAACGGCTACAGATAGCATTCTTAGGACTGACGTGCTGTCTG  
 Bce83I  
 Hpy178III  
 SfcI  
 HinfI  
 TfiI  
 SmlI  
 AluI  
 CviJI  
 AceIII  
 BssSI  
 MnlI  
 TCTCCTAATCAACAATACCTTCGTGGAAACTACAGGAACGAATCTCTCAAGACAAGCTGG  
 2701 -----+-----+-----+-----+-----+ 2760  
 AGAGGATTAGTTGTTATGGAGCACCTTTTGATGTCCTTGCTTAGAGAGTTCTGTTCGACC  
 MboII  
 DpnI  
 Hpy188IX  
 EarI  
 SapI  
 BstYI  
 Sau3AI  
 Hin4I  
 AlwI  
 MaeIII  
 Tsp45I  
 Hpy178III  
 SmlI  
 MnlI  
 MaeIII  
 TATCGGAAGAGCAGGGATCTTTTATGCCTTCTCTCCAAATCTTGAGGTCAACAAGTAACCT  
 2761 -----+-----+-----+-----+-----+ 2820  
 ATAGCCTTCTCGTCCCTAGAAAATACGGAAGAGAGGTTTAGAACTCCAGTGTTTCATTGGA  
 DpnI  
 BstYI  
 Sau3AI  
 MboII  
 ApoI  
 Tsp509I  
 BslI  
 Bce83I  
 AluI  
 CviJI  
 Fnu4HI  
 TseI  
 AlwI  
 DpnI  
 MnlI  
 BglII  
 BstYI  
 Sau3AI  
 BbvI  
 CviRI  
 BsrI  
 ATCTATGGAAATTTCGTGGATCTTCACGCAGCTACAATGCAGATCTTGAGGTAAGTTCCA  
 2821 -----+-----+-----+-----+-----+ 2880  
 TAGATACCTTTAAGCACCTAGAAGTGCCTCGATGTTACGTCTAGAACCTCCATTCAAGGT

[illegible]

Figure 7: Nucleotide and amino acid sequence of CPN100639

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gtacgaagtt cttcacgaaa ttataataca aacctaggct ctaagttttg tttctagatt 60
atcgaaaacg tgttaattaa ttgaacccaa gcacctttct atg aaa ata ccc ttg 115
                                         Met Lys Ile Pro Leu
                                         1           5
cac aaa ctc ctg atc tct tcg act ctt gtc act ccc att cta ttg agc 163
His Lys Leu Leu Ile Ser Ser Thr Leu Val Thr Pro Ile Leu Leu Ser
          10           15           20
att gca act tac gga gca gat gct tct tta tcc cct aca gat agc ttt 211
Ile Ala Thr Tyr Gly Ala Asp Ala Ser Leu Ser Pro Thr Asp Ser Phe
          25           30           35
gat gga gcg ggc ggc tct aca ttt act cca aaa tct aca gca gat gcc 259
Asp Gly Ala Gly Gly Ser Thr Phe Thr Pro Lys Ser Thr Ala Asp Ala
          40           45           50
aat gga acg aac tat gtc tta tca gga aat gtc tat ata aac gat gct 307
Asn Gly Thr Asn Tyr Val Leu Ser Gly Asn Val Tyr Ile Asn Asp Ala
          55           60           65
ggg aaa ggc aca gca tta aca ggc tgc tgc ttt aca gaa act acg ggt 355
Gly Lys Gly Thr Ala Leu Thr Gly Cys Cys Phe Thr Glu Thr Thr Gly
          70           75           80           85
gat ctg aca ttt act gga aag gga tac tca ttt tca ttc aac acg gta 403
Asp Leu Thr Phe Thr Gly Lys Gly Tyr Ser Phe Ser Phe Asn Thr Val
          90           95           100
gat gcg ggt tcg aat gca gga gct gcg gca agc aca act gct gat aaa 451
Asp Ala Gly Ser Asn Ala Gly Ala Ala Ala Ser Thr Thr Ala Asp Lys
          105           110           115
gcc cta atc ttc aca gga ttt tct aac ctt tcc ttc att gca gct cct 499
Ala Leu Ile Phe Thr Gly Phe Ser Asn Leu Ser Phe Ile Ala Ala Pro
          120           125           130
gga act aca gtt gct tca gga aaa agt act tta agt tct gca gga gcc 547
Gly Thr Thr Val Ala Ser Gly Lys Ser Thr Leu Ser Ser Ala Gly Ala
          135           140           145
tta aat ctt acc gat aat gga acg att ctc ttt agc caa aac gtc tcc 595
Leu Asn Leu Thr Asp Asn Gly Thr Ile Leu Phe Ser Gln Asn Val Ser
          150           155           160           165
aat gaa gct aat aac aat ggc gga gcg atc acc aca aaa act ctt tct 643
Asn Glu Ala Asn Asn Asn Gly Gly Ala Ile Thr Thr Lys Thr Leu Ser
          170           175           180
att tct ggg aat acc tct tct ata acc ttc act agt aat agc gca aaa 691
Ile Ser Gly Asn Thr Ser Ser Ile Thr Phe Thr Ser Asn Ser Ala Lys
          185           190           195

```

Fig. 7 (con't)

aaa tta ggt gga gcg atc tat agc tct gcg ggt gca agt att tca gga	739
Lys Leu Gly Gly Ala Ile Tyr Ser Ser Ala Ala Ala Ser Ile Ser Gly	
200 205 210	
aac acc ggc cag tta gtc ttt atg aat aat aaa gga gaa act ggg ggt	787
Asn Thr Gly Gln Leu Val Phe Met Asn Asn Lys Gly Glu Thr Gly Gly	
215 220 225	
ggg gct ctg ggc ttt gaa gcc agc tcc tcg att act caa aat agc tcc	835
Gly Ala Leu Gly Phe Glu Ala Ser Ser Ser Ile Thr Gln Asn Ser Ser	
230 235 240 245	
ctt ttc ttc tct gga aac act gca aca gat gct gca ggc aag ggc ggg	883
Leu Phe Phe Ser Gly Asn Thr Ala Thr Asp Ala Ala Gly Lys Gly Gly	
250 255 260	
gcc att tat tgt gaa aaa aca gga gag act cct act ctt act atc tct	931
Ala Ile Tyr Cys Glu Lys Thr Gly Glu Thr Pro Thr Leu Thr Ile Ser	
265 270 275	
gga aat aaa agt ctg acc ttc gcc gag aac tct tca gta act caa ggc	979
Gly Asn Lys Ser Leu Thr Phe Ala Glu Asn Ser Ser Val Thr Gln Gly	
280 285 290	
gga gca atc tgt gcc cat ggt cta gat ctt tcc gct gct ggc cct acc	1027
Gly Ala Ile Cys Ala His Gly Leu Asp Leu Ser Ala Ala Gly Pro Thr	
295 300 305	
cta ttt tca aat aat aga tgc ggg aac aca gct gca ggc aag ggc ggc	1075
Leu Phe Ser Asn Asn Arg Cys Gly Asn Thr Ala Ala Gly Lys Gly Gly	
310 315 320 325	
gct att gca att gcc gac tct gga tct tta agt ctc tct gca aat caa	1123
Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser Leu Ser Ala Asn Gln	
330 335 340	
gga gac atc acg ttc ctt ggc aac act cta acc tca acc tcc gcg cca	1171
Gly Asp Ile Thr Phe Leu Gly Asn Thr Leu Thr Ser Thr Ser Ala Pro	
345 350 355	
aca tcg aca cgg aat gct atc tac ctg gga tcg tca gca aaa att acg	1219
Thr Ser Thr Arg Asn Ala Ile Tyr Leu Gly Ser Ser Ala Lys Ile Thr	
360 365 370	
aac tta agg gca gcc caa ggc caa tct atc tat ttc tat gat ccg att	1267
Asn Leu Arg Ala Ala Gln Gly Gln Ser Ile Tyr Phe Tyr Asp Pro Ile	
375 380 385	
gca tct aac acc aca gga gct tca gac gtt ctg acc atc aac caa ccg	1315
Ala Ser Asn Thr Thr Gly Ala Ser Asp Val Leu Thr Ile Asn Gln Pro	
390 395 400 405	
gat agc aac tcg cct tta gat tat tca gga acg att gta ttt tct ggg	1363
Asp Ser Asn Ser Pro Leu Asp Tyr Ser Gly Thr Ile Val Phe Ser Gly	
410 415 420	

Fig. 7 (con't)

gaa aag ctc tct gca gat gaa gcg aaa gct gct gat aac ttc aca tct	1411
Glu Lys Leu Ser Ala Asp Glu Ala Lys Ala Ala Asp Asn Phe Thr Ser	
425 430 435	
ata tta aag caa cca ttg gct cta gcc tct gga acc tta gca ctc aaa	1459
Ile Leu Lys Gln Pro Leu Ala Leu Ala Ser Gly Thr Leu Ala Leu Lys	
440 445 450	
gga aat gtc gag tta gat gtc aat ggt ttc aca cag act gaa ggc tct	1507
Gly Asn Val Glu Leu Asp Val Asn Gly Phe Thr Gln Thr Glu Gly Ser	
455 460 465	
aca ctc ctc atg caa cca gga aca aag ctc aaa gca gat act gaa gct	1555
Thr Leu Leu Met Gln Pro Gly Thr Lys Leu Lys Ala Asp Thr Glu Ala	
470 475 480 485	
atc agt ctt acc aaa ctt gtc gtt gat ctt tct gcc tta gag gga aat	1603
Ile Ser Leu Thr Lys Leu Val Val Asp Leu Ser Ala Leu Glu Gly Asn	
490 495 500	
aag agt gtg tcc att gaa aca gca gga gcc aac aaa act ata act cta	1651
Lys Ser Val Ser Ile Glu Thr Ala Gly Ala Asn Lys Thr Ile Thr Leu	
505 510 515	
acc tct cct ctt gtt ttc caa gat agt agc ggc aat ttt tat gaa agc	1699
Thr Ser Pro Leu Val Phe Gln Asp Ser Ser Gly Asn Phe Tyr Glu Ser	
520 525 530	
cat acg ata aac caa gcc ttc acg cag cct ttg gtg gta ttc act gct	1747
His Thr Ile Asn Gln Ala Phe Thr Gln Pro Leu Val Val Phe Thr Ala	
535 540 545	
gct act gct gct agc gat att tat atc gat gcg ctt ctc act tct cca	1795
Ala Thr Ala Ala Ser Asp Ile Tyr Ile Asp Ala Leu Leu Thr Ser Pro	
550 555 560 565	
gta caa act cca gaa cct cat tac ggg tat cag gga cat tgg gaa gcc	1843
Val Gln Thr Pro Glu Pro His Tyr Gly Tyr Gln Gly His Trp Glu Ala	
570 575 580	
act tgg gca gac aca tca act gca aaa tca gga act atg act tgg gta	1891
Thr Trp Ala Asp Thr Ser Thr Ala Lys Ser Gly Thr Met Thr Trp Val	
585 590 595	
act acg ggc tac aac cct aat cct gag cgt aga gct tcc gta gtt ccc	1939
Thr Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Ala Ser Val Val Pro	
600 605 610	
gat tca tta tgg gca tcc ttt act gac att cgc act cta cag cag atc	1987
Asp Ser Leu Trp Ala Ser Phe Thr Asp Ile Arg Thr Leu Gln Gln Ile	
615 620 625	
atg aca tct caa gcg aat agt atc tat cag caa cga gga ctc tgg gca	2035
Met Thr Ser Gln Ala Asn Ser Ile Tyr Gln Arg Gly Leu Trp Ala	
630 635 640 645	

Fig. 7 (con't)

tca gga act gcg aat ttc ttc cat aag gat aaa tca gga act aac caa	2083
Ser Gly Thr Ala Asn Phe Phe His Lys Asp Lys Ser Gly Thr Asn Gln	
650 655 660	
gca ttc cga cat aaa agc tac ggc tat att gtt gga gga agt gct gaa	2131
Ala Phe Arg His Lys Ser Tyr Gly Tyr Ile Val Gly Gly Ser Ala Glu	
665 670 675	
gat ttt tct gaa aat atc ttc agt gta gct ttc tgc cag ctc ttc ggt	2179
Asp Phe Ser Glu Asn Ile Phe Ser Val Ala Phe Cys Gln Leu Phe Gly	
680 685 690	
aaa gat aaa gac ctg ttt ata gtt gaa aat acc tct cat aac tat tta	2227
Lys Asp Lys Asp Leu Phe Ile Val Glu Asn Thr Ser His Asn Tyr Leu	
695 700 705	
gcg tcg cta tac ctg caa cat cga gca ttc cta gga gga ctt ccc atg	2275
Ala Ser Leu Tyr Leu Gln His Arg Ala Phe Leu Gly Gly Leu Pro Met	
710 715 720 725	
ccc tca ttt gga agt atc acc gac atg ctg aaa gat att cct ctc att	2323
Pro Ser Phe Gly Ser Ile Thr Asp Met Leu Lys Asp Ile Pro Leu Ile	
730 735 740	
ttg aat gcc cag cta agc tac agc tac act aaa aat gat atg gat act	2371
Leu Asn Ala Gln Leu Ser Tyr Ser Tyr Thr Lys Asn Asp Met Asp Thr	
745 750 755	
cgc tat act tcc tat cct gaa gct caa ggc tct tgg acc aat aac tct	2419
Arg Tyr Thr Ser Tyr Pro Glu Ala Gln Gly Ser Trp Thr Asn Asn Ser	
760 765 770	
ggg gct cta gag ctc gga gga tct ctg gct cta tat ctc cct aaa gaa	2467
Gly Ala Leu Glu Leu Gly Gly Ser Leu Ala Leu Tyr Leu Pro Lys Glu	
775 780 785	
gca ccg ttc ttc cag gga tat ttc ccc ttc tta aag ttc cag gca gtc	2515
Ala Pro Phe Phe Gln Gly Tyr Phe Pro Phe Leu Lys Phe Gln Ala Val	
790 795 800 805	
tac agc cgc caa caa aac ttt aaa gag agt ggc gct gaa gcc cgt gct	2563
Tyr Ser Arg Gln Gln Asn Phe Lys Glu Ser Gly Ala Glu Ala Arg Ala	
810 815 820	
ttt gat gat gga gac cta gtg aac tgc tct atc cct gtc ggc att cgg	2611
Phe Asp Asp Gly Asp Leu Val Asn Cys Ser Ile Pro Val Gly Ile Arg	
825 830 835	
tta gaa aaa atc tcc gaa gat gaa aaa aat aat ttc gag att tct cta	2659
Leu Glu Lys Ile Ser Glu Asp Glu Lys Asn Asn Phe Glu Ile Ser Leu	
840 845 850	
gcc tac att ggt gat gtg tat cgt aaa aat ccc cgt tcg cgt act tct	2707
Ala Tyr Ile Gly Asp Val Tyr Arg Lys Asn Pro Arg Ser Arg Thr Ser	
855 860 865	

Fig. 7 (con't)

```

cta atg gtc agt gga gcc tct tgg act tcg cta tgt aaa aac ctc gca 2755
Leu Met Val Ser Gly Ala Ser Trp Thr Ser Leu Cys Lys Asn Leu Ala
870                      875                      880                      885

cga caa gcc ttc tta gca agt gct gga agc cat ctg act ctc tcc cct 2803
Arg Gln Ala Phe Leu Ala Ser Ala Gly Ser His Leu Thr Leu Ser Pro
                        890                      895                      900

cat gta gaa ctc tct ggg gaa gct gct tat gag ctt cgt ggc tca gca 2851
His Val Glu Leu Ser Gly Glu Ala Ala Tyr Glu Leu Arg Gly Ser Ala
                        905                      910                      915

cac atc tac aat gta gat tgt ggg cta aga tac tca ttc tagttcctac 2900
His Ile Tyr Asn Val Asp Cys Gly Leu Arg Tyr Ser Phe
                        920                      925                      930

tttcctccct aaacttttag ggaggaattc ttataaaaac cctgtagatt cttaacttac 2960

tagtctctcc tttcctcttg ctttctttaa tttattgcag 3000

```

Figure 8: Restriction enzyme analysis of CPN100639

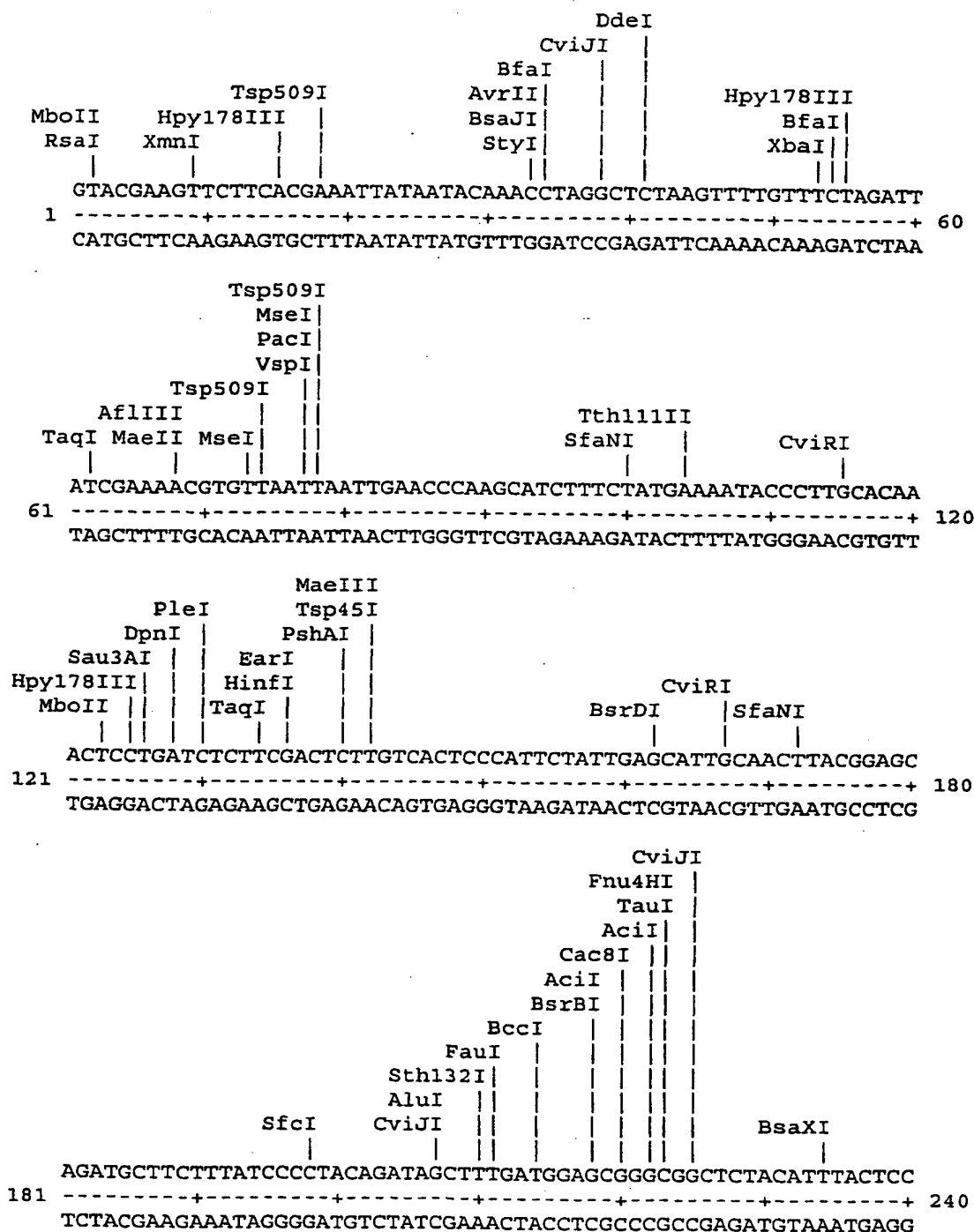




Fig. 8 (con't)

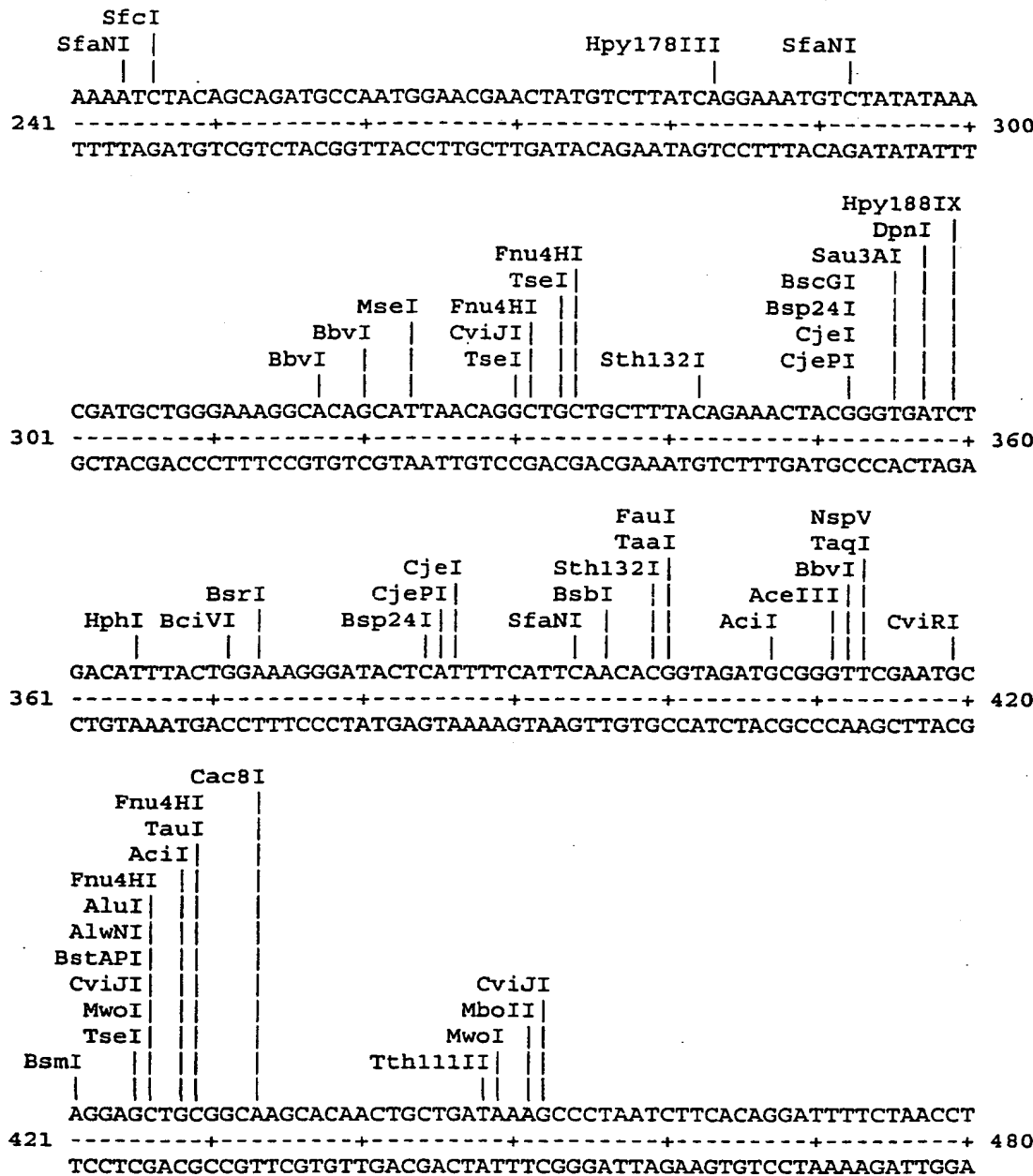
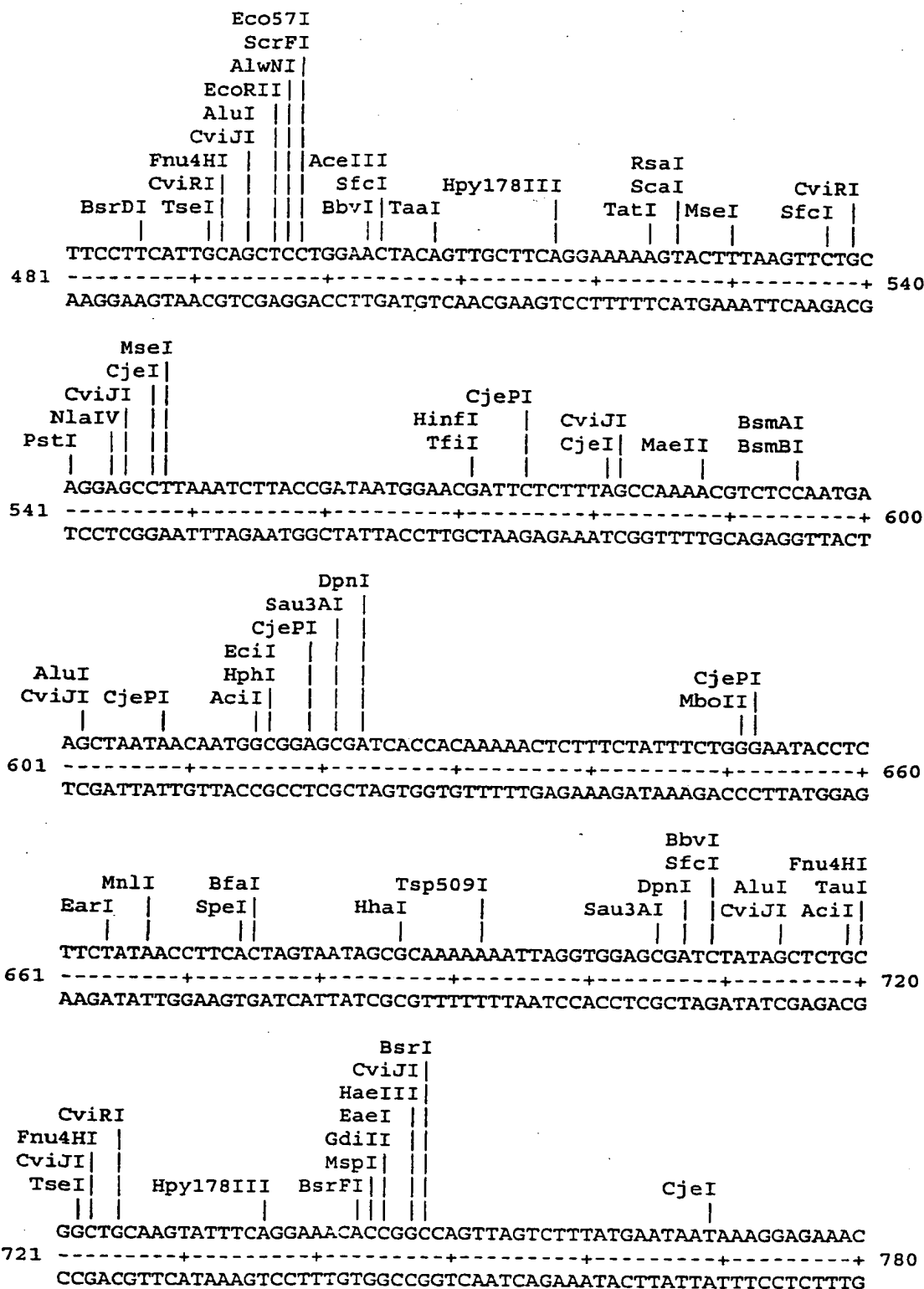


Fig. 8 (con't)



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CviJI  
Cac8I  
CviJI  
BanII  
CjeI  
BsrI  
Bsp1286I  
BseRI  
MnlI  
AceIII  
MboII  
AluI  
CviJI  
TaqI  
BmrI

781

ACCCCCACCCCGAGACCCGAACTTCGGTCGAGGAGCTAATGAGTTTATCGAGGGAAAA

FauI  
Cac8I  
PstI  
Sth132I  
CviRI  
Pnu4HI  
SfcI  
AlwNI  
TseI  
BstAPI  
TspRI  
CviRI  
BtsI  
BbvI  
Hpy178III  
SfaNI  
MwoI  
CviJI  
HaeIII  
NlaIV  
Sau96I  
AciI  
CjeI

841

GAAGAGACCTTTGTGACGTTGTCTACGACGTCCGTTCCCGCCCCGGTAAATAACACTTTT

Hin4I  
CjeI  
PleI  
CjeI  
BsmAI  
HinfI  
Hpy178III  
Eco57I  
CjeI  
Hpy188IX  
Bce83I  
MboII

901

TGTGCTCTCTGAGGATGAGAATGATAGAGACCTTTATTTTCAGACTGGAAGCGGCTCTT

[illegible]

Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA  
FRAGMENTS AND USES THEREOF  
Inventor(s): Andrew D. MURDIN et al.  
DOCKET NO.: 032931-0252

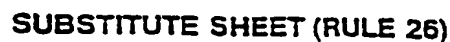


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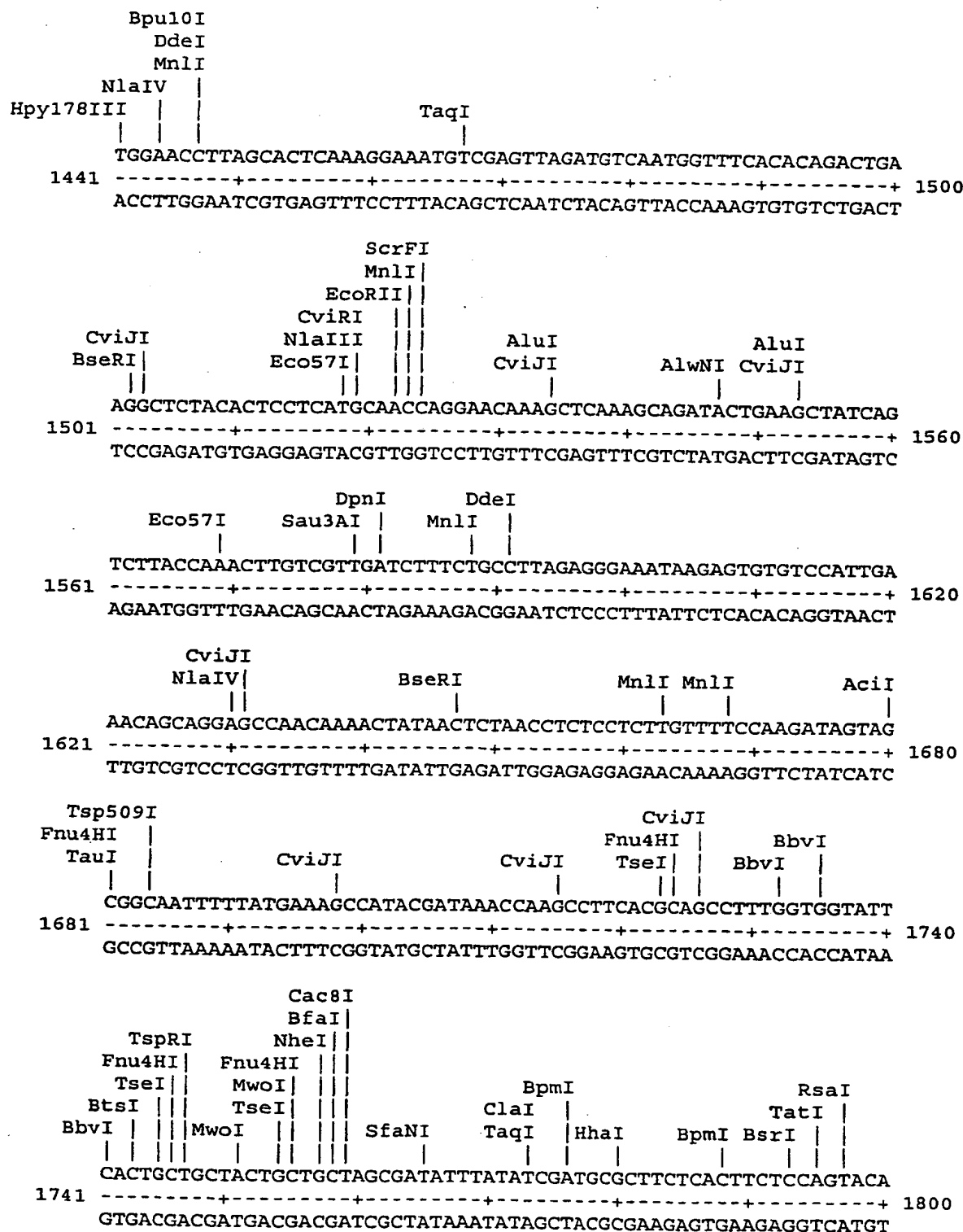


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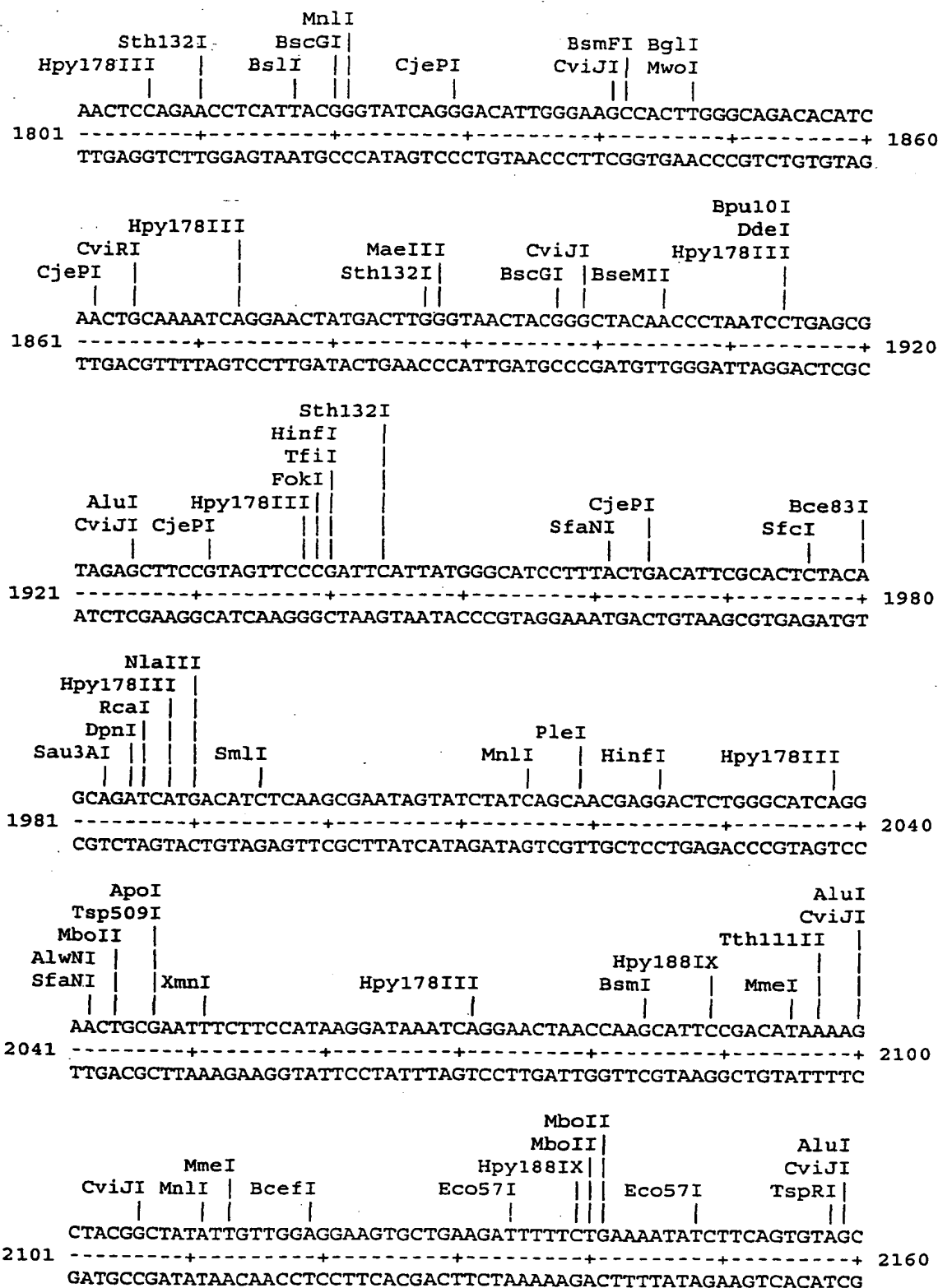


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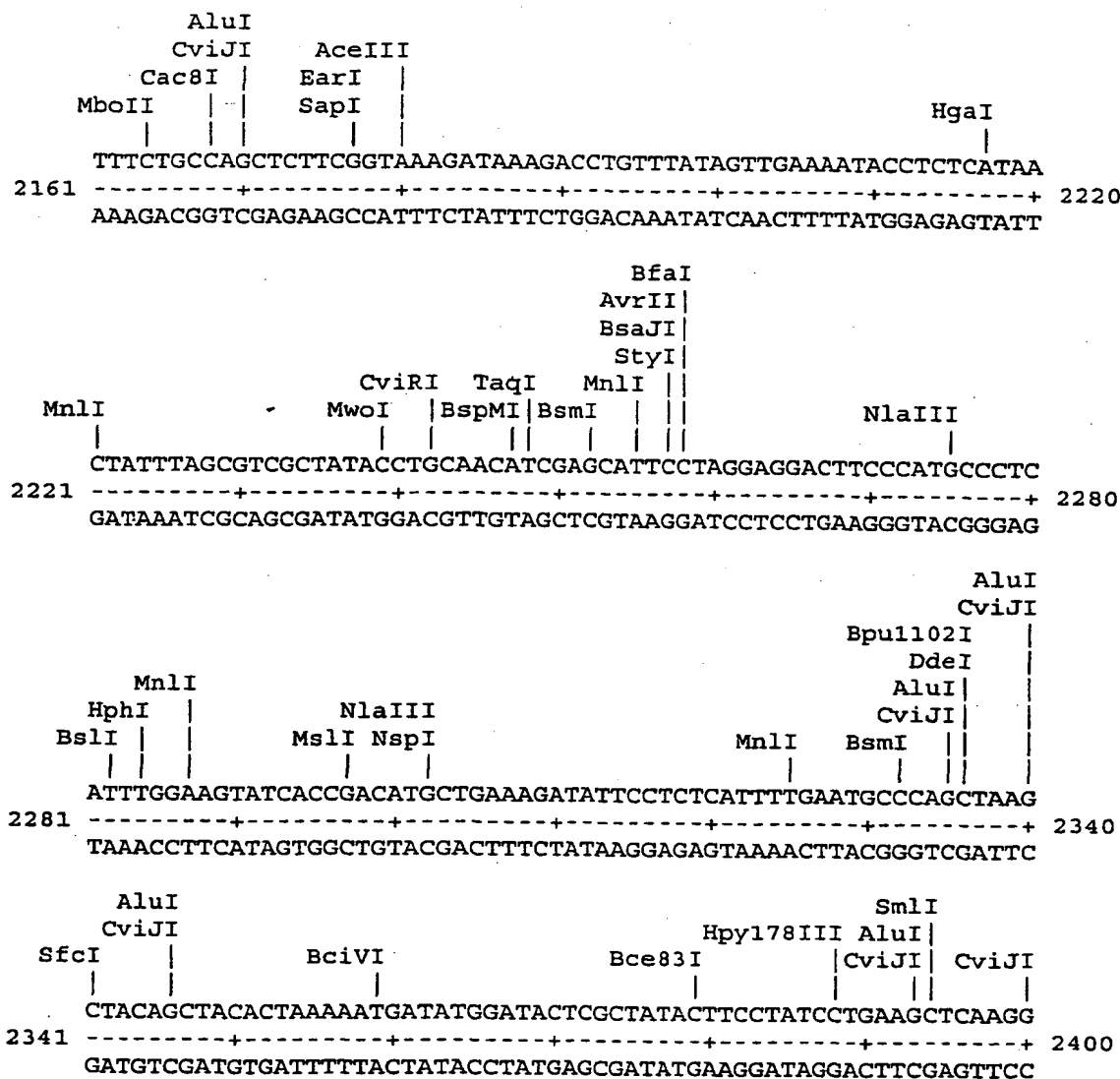




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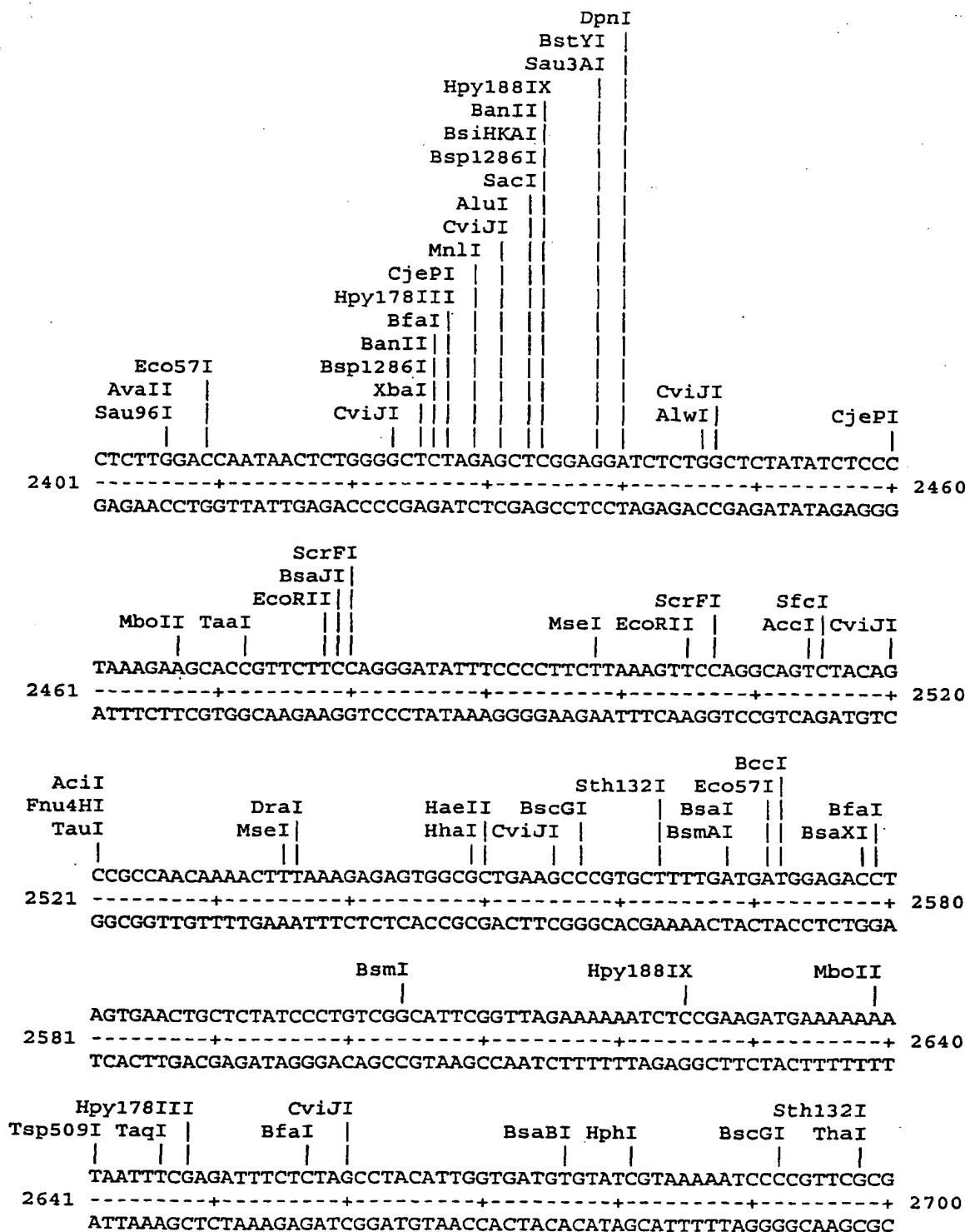


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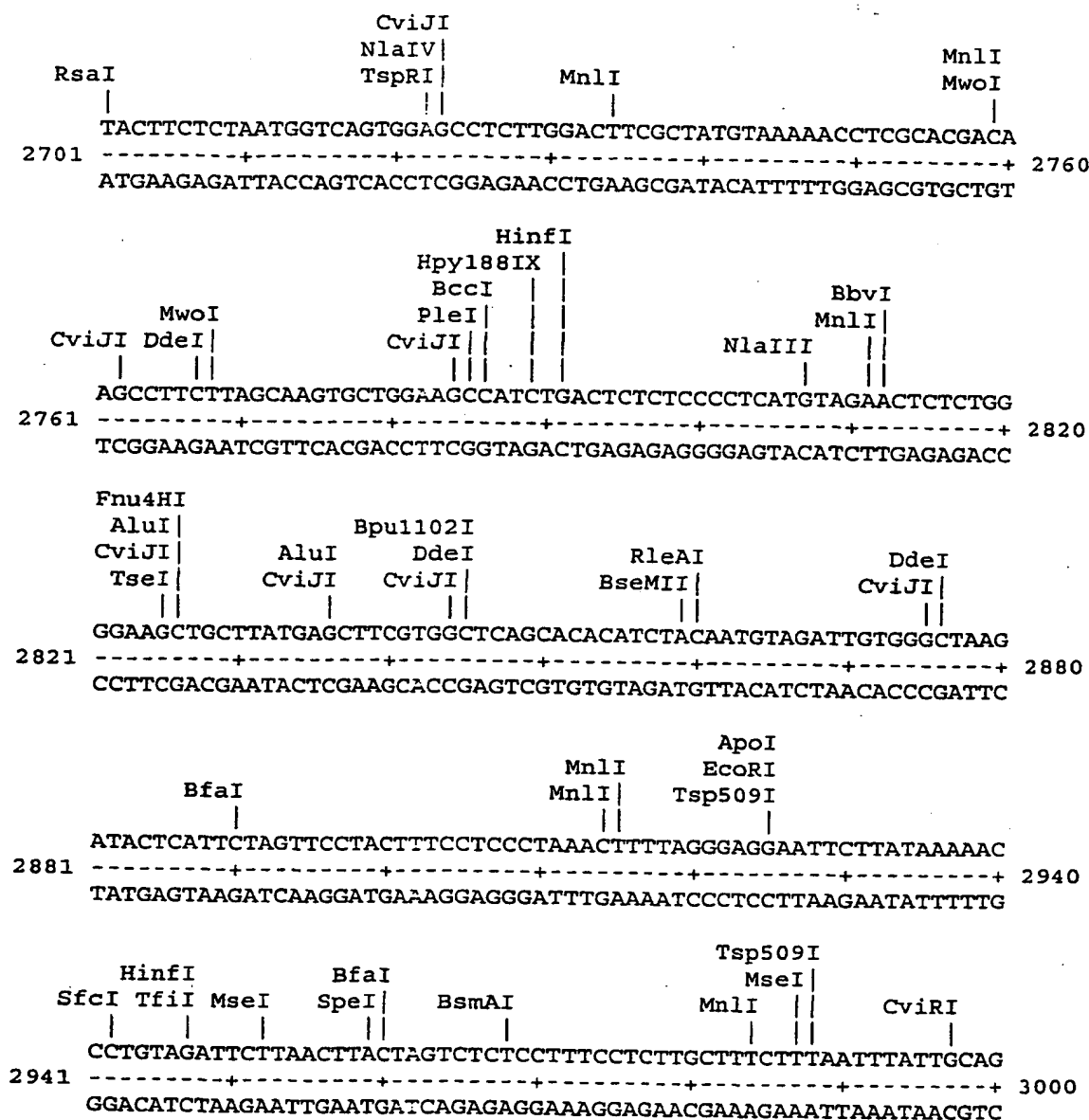


Figure 9: Nucleotide and amino acid sequence of CPN100708

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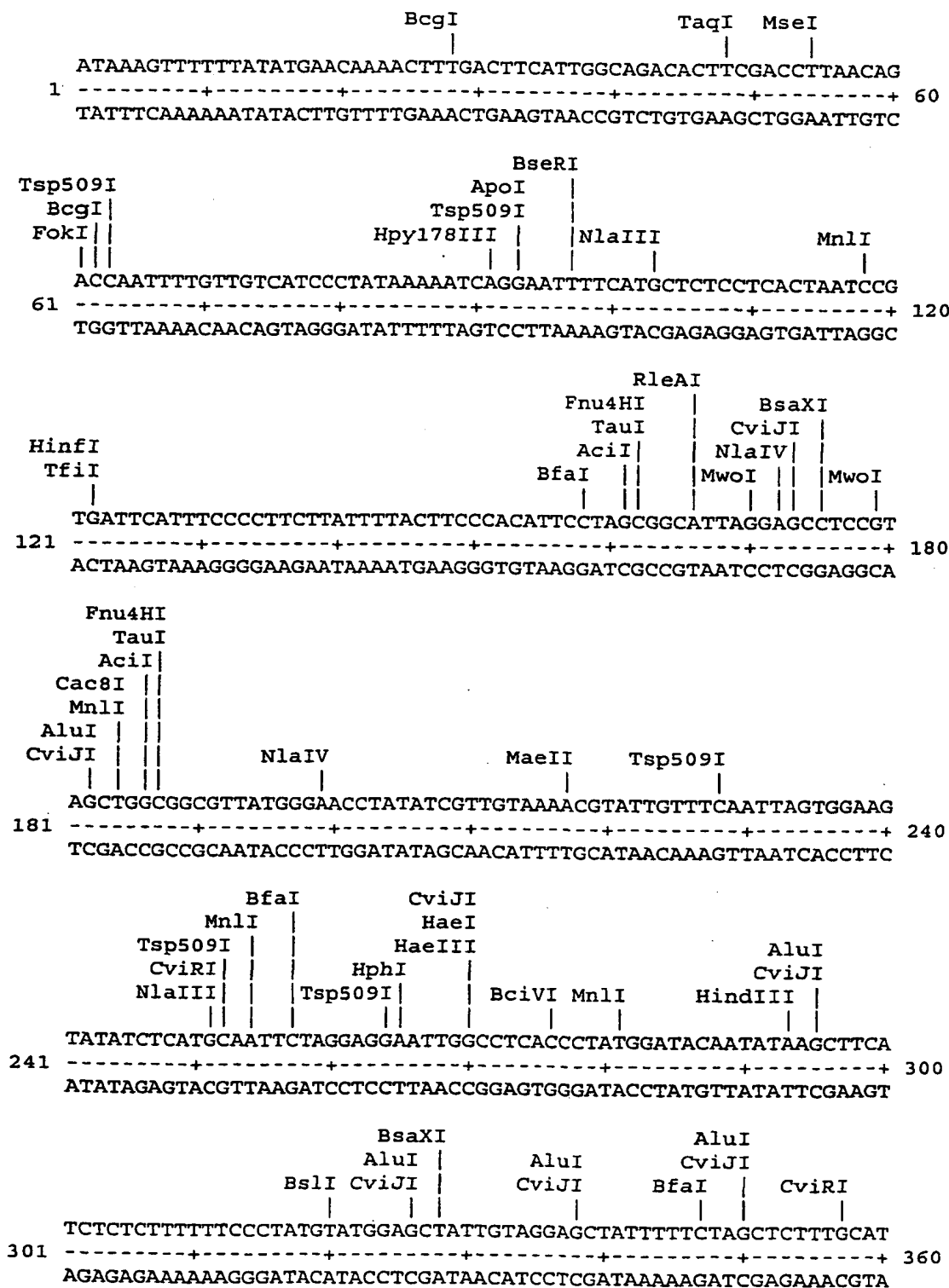
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                                     Met Leu Ser Ser Leu
                                     1 5
atc cgt gat tca ttt ccc ctt ctt att tta ctt ccc aca ttc cta gcg 163
Ile Arg Asp Ser Phe Pro Leu Leu Ile Leu Leu Pro Thr Phe Leu Ala
                                     10 15 20
gca tta gga gcc tcc gta gct ggc ggc gtt atg gga acc tat atc gtt 211
Ala Leu Gly Ala Ser Val Ala Gly Gly Val Met Gly Thr Tyr Ile Val
                                     25 30 35
gta aaa cgt att gtt tca att agt gga agt ata tct cat gca att cta 259
Val Lys Arg Ile Val Ser Ile Ser Gly Ser Ile Ser His Ala Ile Leu
                                     40 45 50
gga gga att ggc ctc acc cta tgg ata caa tat aag ctt cat ctc tct 307
Gly Gly Ile Gly Leu Thr Leu Trp Ile Gln Tyr Lys Leu His Leu Ser
                                     55 60 65
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Phe Phe Pro Met Tyr Gly Ala Ile Val Gly Ala Ile Phe Leu Ala Leu
                                     70 75 80 85
tgc atc ggc aag atc cac ctg aaa tac caa gaa agg gaa gac tct ttg 403
Cys Ile Gly Lys Ile His Leu Lys Tyr Gln Glu Arg Glu Asp Ser Leu
                                     90 95 100
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Ile Ala Met Ile Trp Ser Val Gly Met Ala Ile Gly Ile Ile Phe Ile
                                     105 110 115
tcc agg ctt ccc acc ttt aat gga gag ctc atc aat ttt cta ttt ggg 499
Ser Arg Leu Pro Thr Phe Asn Gly Glu Leu Ile Asn Phe Leu Phe Gly
                                     120 125 130
aac att ctc tgg gtc acc cct tca gac ctc tat agc tta gga atc ttt 547
Asn Ile Leu Trp Val Thr Pro Ser Asp Leu Tyr Ser Leu Gly Ile Phe
                                     135 140 145
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Asp Leu Leu Val Leu Gly Ile Val Val Leu Cys His Thr Arg Phe Leu
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gct ctt tgc ttt gat gag agg tac acg gct tta aac cat tgt tct gta 643
Ala Leu Cys Phe Asp Glu Arg Tyr Thr Ala Leu Asn His Cys Ser Val
                                     170 175 180
cag ctg tgg tat ttc cta ctt ctt gtt ctg aca gca atc acg att gtg 691
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Fig. 9 (con't)

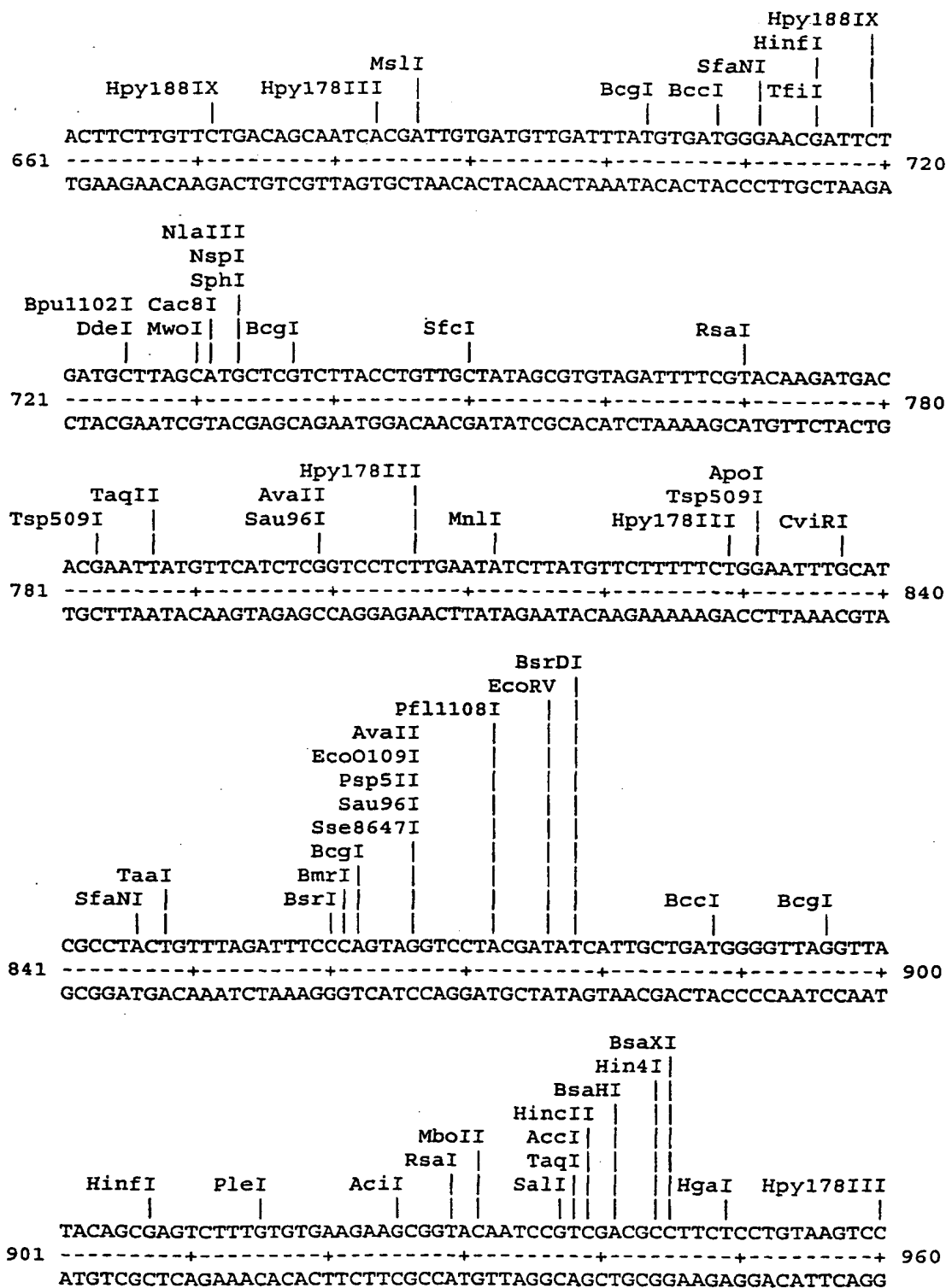
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Leu Pro Val Ala Ile Ala Cys Arg Phe Ser Tyr Lys Met Thr Arg Ile	
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Met Phe Ile Ser Val Leu Leu Asn Ile Leu Cys Ser Phe Ser Gly Ile	
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tgc atc gcc tac tgt tta gat ttc cca gta ggt cct acg ata tca ttg	883
Cys Ile Ala Tyr Cys Leu Asp Phe Pro Val Gly Pro Thr Ile Ser Leu	
250 255 260	
ctg atg ggg tta ggt tat aca gcg agt ctt tgt gtg aag aag cgg tac	931
Leu Met Gly Leu Gly Tyr Thr Ala Ser Leu Cys Val Lys Lys Arg Tyr	
265 270 275	
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Asn Pro Ser Thr Pro Ser Pro Val Ser Pro Glu Ile Asn Thr Asn Val	
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tcatacaattt tatttaaagc taccagcata tctttctttt caaaatctgg ctgatgagag	1099
t	1100

Figure 10: Restriction enzyme analysis of CPN100708



**SUBSTITUTE SHEET (RULE 26)**

Fig. 10 (con't)



**SUBSTITUTE SHEET (RULE 26)**



Figure 11: Identification of T- and B- cell epitopes from open reading frame ORF:  
cpn100634 (SEQ ID NO: 11)

```

1 MKTSIPWVLV SSVLAFSCHL QSLANEELLS PDDSFNGNID SGTFTPKTSA
51 TTYSLTGDVF FYEPGKGTP L SDSCFKQTTD NLTF LGNGHS LTFG FIDAGT
101 HAGAASTTA NKNLTFSGFS LLSFDSSPST TVTTGQGTLS SAGGVNLENI
151 RKLVVAGNFS TADGGAIKGA SFLLTGTSGD ALFSNNSSST KGGAIATTAG
201 ARIANNTGYV RFLSNIASTS GGAI DDEGTS ILSNNKFLYF EGNAAKTTGG
251 AICNTKASGS PELIISNNKT LIFASNVAET SGGAIHAKKL ALSSGGFTEF
301 LRNNVSSATP KGGAISIDAS GELSLSAETG NITFVRNTLT TTGSTDTPKR
351 NAINIGSNGK FTELRAAKNH TIFYDPI TS EGTSSDVLKI NNGSAGALNP
401 YQGTILFSGE TLTADELKVA DN LKSSFTQP VSLSGGKLLL QKGV TLEST S
451 FSQEAGSLLG MDSGTTLSTT AGSITITNLG INVDSLGLKQ PVSLTAKGAS
501 NKVIVSGKLN LIDIEGNIYE SHMF SHDQLF SLLKITVDAD VDTNVDISSL
551 IPVPAEDPNS EYGFQGWNV NWT TDTATNT KEATATWTKT GFVPSPERKS
601 ALVCNTLWGV FTDIRSLQQL VEIGATGMEH KQGFVSSMT NFLHKTGDEN
651 RKGFRHTSGG YVIGGSAHTP KDDLFTFAFC HLFARDKDCF IAHNNSRTYG
701 GTLFFKHSHT LQPQNYLR LG RAKFSESAIE KFPREIPLAL DVQVSFSHSD
751 NRMETHYTS L PESEGSWSNE CIAGGIGLDL PFVLSNPHPL FKTFIPQMKV
801 EMVYVSQNSF FESSSDGRGF SIGRLLNLSI PVGAKFVQGD IGDSYTYDLS
851 GFFVSDVYRN NPQSTATLVM SPDSWKIRGG NLSRQAFLLR GSN NYVYNSN
901 CELFGHYAME LRGSSRNYNV DVGTKLRF

```

Possible T cell epitope:

824 RLLNLSIPV

Possible B cell epitope:

644 HKTGDENRKGFRHTS

Figure 12: Identification of T- and B- cell epitopes from open reading frame ORF:  
cpn100635 (SEQ ID.NO: 12)

```

1  MKSQFSWLVL SSTLACFTSC STVFAATAEN IGPSDSFDGS TNTGTYTPKN
51 TTTGIDYTLT GDITLQNLGD SAALTGKCFs DTESLSFAG KGYSLSFLNI
101 KSSAEGAALS VTDDKNLSLT GFSSLTFLAA PSSVITTPSG KGAVKCGGDL
151 TFDNNGTILF KQDYCEENG AISTKNLSLK NSTGSISFEG NKSSATGKKG
201 GAICATGTVD ITNNTAPTIF SNNIAEAAGG AINSTGNCTI TGNTSLVFSE
251 NSVTATAGNG GALSGDADVT ISGNQSVTFS GNQAVANGGA IYAKKLTLAS
301 GGGGGNPFSS NIVQGTAGN GGAISILAAG ECSLFSEAGD HYLNGNAIVA
351 TTPQTTKRNS IDIGSTGKDH ELRAISGHSI FFYDPITANT AADSTDTLNL
401 NKADAGNSTD YSGSIVFSGE KLSEDEAKVA DNLTSTLKQP VTLTAGNLVL
451 KRGVTLDTKG FTQTAGSSVI MDAGTTLKAS TEEVTLTGLS IPVDSLGEGK
501 KVVIAASAAS KVALSGPIL LLDNQGNAYE NHDLGKTQDF SFVQLSALGT
551 ATTTDVPAPV TVATPTHYGY QGTWGMTWVD DTASTPKTKT ATLAWTNTGY
601 LPNPERQGPL VPNSLWGSFS DIQAIQGVIE RSALTLCSDR GFWAAGVANF
651 LDKDKKGEKR KYRHKSGGYA IGGAAQTCSE NLISFAFCQL FGSDKDFLVA
701 KNHTDTYAGA FYIQHITECS GFIGCLLDKL PGWSHKPLV LEGQLAYSHV
751 SNDLKTKYTA YPEVKGSWGN NAFNMMLGAS SHSYPEYLHC FDTYAPYIKL
801 NLTYIRQDSF SEKGTEGRSF DDSNLFNLSL PIGVKFEKFS DCNDFS YDLT
851 LSYVPDLIRN DPKCTTALVI SGASWET YAN NLARQALQVR AGSHYAFSPM
901 FEVLGQFVFE VRGSSRIYNV DLGGKFQF

```

Possible T cell epitope:

903 VLGQFVFEV

Possible B cell epitope:

DKDKKGEKRKYRHKSG

Figure 13: Identification of T- and B- cell epitopes from open reading frame ORF:  
cpn100638 (SEQ ID NO: 14)

1	MKSSLHWFLI	SSSLALPLSL	NFSAFAAVVE	INLGPTNSFS	GPGTYTPPAQ
51	TTNADGTIYN	LTGDVSITNA	GSPTALTASC	FKETTGNLSF	QGHGYQFLLQ
101	NIDAGANCTF	TNTAANKLLS	FSGFSYLSLI	QTTNATTGTG	AIKSTGACSI
151	QSNYSCYFGQ	NFSNDNGGAL	QGSSISLSLN	PNLTFAKNKA	TQKGGALYST
201	GGITINNTLN	SASFSENTAA	NNGGAIYTEA	SSFISSNKAI	SFINNSVTAT
251	SATGGAIYCS	STSAPKPVLT	LSDNCELNFI	GNTAITSGGA	IYTDNLVLSS
301	GGPTLFFKNNS	GYDTAAPLGG	AIAIADSGSL	SLSALGGDIT	FEGNTVVKGA
351	SSSQTTTRNS	INIGNTNAKI	VQLRASQGNT	IYFYDPITTS	ITAALSDALN
401	LNGPDLAGNP	AYQGTIVFSG	EKLSEAEAAE	ADNLKSTIQQ	PLTLAGGQLS
451	LKSGVTLVAK	SFSQSPGSTL	LMDAGTTLET	ADGITINNLV	LNVDLSLKETK
501	KGTLKATQAS	QTVTLSGSLS	LVDPSGNVYE	DVSWNNPQVF	SCLTLTADDP
551	ANIHITDLAA	DPLEKNPIHW	GYQGNWALSW	QEDTATKSKA	ATLTWTKTGY
601	NPNPERRGTL	VANTLWGSFV	DVRSIQQLVA	TKVRQSQETR	GIWCEGISNF
651	FHKDSTKINK	GFRHISAGYV	VGATTTLASD	NLITAAFCQL	FGKDRDHFIN
701	KNRASAYAAS	LHLQHLATLS	SPSLLRYLPG	SESEQPVLFD	AQISYIYSKN
751	TMKTYYTQAP	KGESSWYNDG	CALELASSLP	HTALSHEGLF	HAYFPFIKVE
801	ASYIHQDSFK	ERNTTLVRSF	DSGDLINVSF	PIGITFERFS	RNERASYEAT
851	VIYVADVYRK	NPDCTTALLI	NNTSWKTTGT	NLSRQAGIGR	AGIFYAFSPN
901	LEVTSNLSME	IRGSSRSYNA	DLGGKFQF		

Possible T cell epitope:

614 TLWGSFVDV

Possible B cell epitope:

595 WTKTGYNPNPERRG

Figure 14: Identification of T- and B- cell epitopes from open reading frame ORF:  
cpn100639 (SEQ ID NO: 15)

1	MKIPLHKLLI	SSTLVTPILL	SIATYGADAS	LSPTDSFDGA	GGSTFTPCKST
51	ADANGTNYVL	SGNVYINDAG	KGTALTGCCF	TETTGDLTFT	GKGYSFSFNT
101	VDAGSNAGAA	ASTTADKALI	FTGFSNLSFI	AAPGTTVASG	KSTLSSAGAL
151	NLTDNGTILF	SQNVSNNEANN	NGGAITTKTL	SISGNTSSIT	FTSNSAKKLG
201	GAIYSSAAAS	ISGNTGQLVF	MNNKGETGGG	ALGFEASSSI	TQNSSLFFSG
251	NTATDAAGKG	GAIYCEKTGE	TPTLTISGNK	SLTFAENSSV	TQGGAI CAHG
301	LDLSAAGPTL	FSNNRCGNTA	AGKGGAI AIA	DSGSLSLSAN	QGDITFLGNT
351	LTSTSAPTST	RNAIYLGSSA	KITNLRAAQG	QSIYFYDPIA	SNTTGASDVL
401	TINQPDSNSP	LDYSGTIVFS	GEKLSADEAK	AADNFTSILK	QPLALASGTL
451	ALKGNVELDV	NGFTQTEGST	LLMQPGTKLK	ADTEAISLTK	LVVDLSALEG
501	NKSVSIETAG	ANKTITLTSP	LVFQDSSGNF	YESHTINQAF	TQPLVVFTAA
551	TAASDIYIDA	LLTSPVQTPE	PHYGYQGHWE	ATWADTSTAK	SGTMTWVTTG
601	YNPNPERRAS	VVPDSLWASF	TDIRTLQQIM	TSQANSIYQQ	RGLWASGTAN
651	FFHKDKSGTN	QAFRHKSYGY	IVGGS AEDFS	ENIFSVAF CQ	LFGKDKDLFI
701	VENTSHNYLA	SLYLQHRAFL	GGLPMPSFGS	ITDMLKDIPL	ILNAQLSYSY
751	TKNDMDTRYT	SYPEAQGSWT	NNSGALELGG	SLALYLPKEA	PFFQGYFPFL
801	KFQAVYSRQQ	NFKESGAEAR	AFDDGDLVNC	SIPVGIRLEK	ISEDEKNNFE
851	ISLAYIGDVY	RKNPRSRTSL	MVSGASWTSL	CKNLARQAFL	ASAGSHLTLS
901	PHVELSGEAA	YELRGS AHY	NVDCGLRYSF		

Possible T cell epitope:

7 KLLISSTLV

Possible B cell epitopes:

839 EKISEDEKNNF

860 YRKNPRSRT

Figure 15: Identification of T- and B- cell epitopes from open reading frame ORF:  
cpn100708 (SEQ ID NO: 16)

1 MLSSLIRDSF PLLILLPTFL AALGASVAGG VMGTIYIVVKR IVSISGSISH  
51 AILGGIGLTL WIQYKLHLSF FPMYGAIVGA IFLALCIGKI HLKYQEREDS  
101 LIAMIWSVGM AIGIIFISRL PTFNGELINF LFGNILWVTP SDLYSLGIFD  
151 LLVLGIVVLC HTRFLALCFD ERYTALNHCS VQLWYFLLLV LTAITIVMLI  
201 YVMGTILMLS MLVLPVAIAC RFSYKMTRIM FISVLLNILC SFSGICIAYC  
251 LDFFVGPPTIS LLMGLGYTAS LCVKKRYNPS TPSPVSPEIN TNV

Possible T cell epitope:

130 FLFGNILWV

Possible B cell epitope:

91 HLKYQEREDS

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1 5  
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Pro Trp Val Leu Val Ser Ser Val Leu Ala Phe Ser Cys His Leu Gln  
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Asn Ile Asp Ser Gly Thr Phe Thr Pro Lys Thr Ser Ala Thr Thr Tyr  
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Ser Leu Thr Gly Asp Val Phe Phe Tyr Glu Pro Gly Lys Gly Thr Pro  
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Leu Ser Asp Ser Cys Phe Lys Gln Thr Thr Asp Asn Leu Thr Phe Leu  
70 75 80 85  
ggg aac ggt cat agc tta acg ttt ggc ttt ata gat gct ggc act cat 403  
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90 95 100

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Gly Phe Ser Leu Leu Ser Phe Asp Ser Ser Pro Ser Thr Val Thr	
120 125 130	
aca ggt cag gga acg ctt tcc tca gca gga ggc gta aat tta gaa aat	547
Thr Gly Gln Gly Thr Leu Ser Ser Ala Gly Gly Val Asn Leu Glu Asn	
135 140 145	
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Ile Arg Lys Leu Val Val Ala Gly Asn Phe Ser Thr Ala Asp Gly Gly	
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Ala Ile Lys Gly Ala Ser Phe Leu Leu Thr Gly Thr Ser Gly Asp Ala	
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Ile Asn Asn Gly Ser Ala Gly Ala Leu Asn Pro Tyr Gln Gly Thr Ile	
390 395 400 405	
cta ttt tct gga gaa acc cta aca gca gat gaa ctt aaa gtt gct gac	1363
Leu Phe Ser Gly Glu Thr Leu Thr Ala Asp Glu Leu Lys Val Ala Asp	
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WO 00/32794

Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA  
FRAGMENTS AND USES THEREOF  
Inventor(s): Andrew D. MURDIN et al.  
DOCKET NO.: 032931-0252

09/857128

PCT/CA99/01147

Asn Thr Leu Thr Thr Thr Gly Ser Thr Asp Thr Pro Lys Arg Asn Ala  
340 345 350

Ile Asn Ile Gly Ser Asn Gly Lys Phe Thr Glu Leu Arg Ala Ala Lys  
355 360 365

Asn His Thr Ile Phe Phe Tyr Asp Pro Ile Thr Ser Glu Gly Thr Ser  
370 375 380

Ser Asp Val Leu Lys Ile Asn Asn Gly Ser Ala Gly Ala Leu Asn Pro  
385 390 395 400

Tyr Gln Gly Thr Ile Leu Phe Ser Gly Glu Thr Leu Thr Ala Asp Glu  
405 410 415

Leu Lys Val Ala Asp Asn Leu Lys Ser Ser Phe Thr Gln Pro Val Ser  
420 425 430

Leu Ser Gly Gly Lys Leu Leu Leu Gln Lys Gly Val Thr Leu Glu Ser  
435 440 445

Thr Ser Phe Ser Gln Glu Ala Gly Ser Leu Leu Gly Met Asp Ser Gly  
450 455 460

Thr Thr Leu Ser Thr Thr Ala Gly Ser Ile Thr Ile Thr Asn Leu Gly  
465 470 475 480

Ile Asn Val Asp Ser Leu Gly Leu Lys Gln Pro Val Ser Leu Thr Ala  
485 490 495

Lys Gly Ala Ser Asn Lys Val Ile Val Ser Gly Lys Leu Asn Leu Ile  
500 505 510

Asp Ile Glu Gly Asn Ile Tyr Glu Ser His Met Phe Ser His Asp Gln  
515 520 525

Leu Phe Ser Leu Leu Lys Ile Thr Val Asp Ala Asp Val Asp Thr Asn  
530 535 540

Val Asp Ile Ser Ser Leu Ile Pro Val Pro Ala Glu Asp Pro Asn Ser  
545 550 555 560

Glu Tyr Gly Phe Gln Gly Gln Trp Asn Val Asn Trp Thr Thr Asp Thr  
565 570 575

Ala Thr Asn Thr Lys Glu Ala Thr Ala Thr Trp Thr Lys Thr Gly Phe  
580 585 590

Val Pro Ser Pro Glu Arg Lys Ser Ala Leu Val Cys Asn Thr Leu Trp  
595 600 605

Gly Val Phe Thr Asp Ile Arg Ser Leu Gln Gln Leu Val Glu Ile Gly  
610 615 620

Ala Thr Gly Met Glu His Lys Gln Gly Phe Trp Val Ser Ser Met Thr  
625 630 635 640



Asn Phe Leu His Lys Thr Gly Asp Glu Asn Arg Lys Gly Phe Arg His  
 645 650 655  
 Thr Ser Gly Gly Tyr Val Ile Gly Gly Ser Ala His Thr Pro Lys Asp  
 660 665 670  
 Asp Leu Phe Thr Phe Ala Phe Cys His Leu Phe Ala Arg Asp Lys Asp  
 675 680 685  
 Cys Phe Ile Ala His Asn Asn Ser Arg Thr Tyr Gly Gly Thr Leu Phe  
 690 695 700  
 Phe Lys His Ser His Thr Leu Gln Pro Gln Asn Tyr Leu Arg Leu Gly  
 705 710 715 720  
 Arg Ala Lys Phe Ser Glu Ser Ala Ile Glu Lys Phe Pro Arg Glu Ile  
 725 730 735  
 Pro Leu Ala Leu Asp Val Gln Val Ser Phe Ser His Ser Asp Asn Arg  
 740 745 750  
 Met Glu Thr His Tyr Thr Ser Leu Pro Glu Ser Glu Gly Ser Trp Ser  
 755 760 765  
 Asn Glu Cys Ile Ala Gly Gly Ile Gly Leu Asp Leu Pro Phe Val Leu  
 770 775 780  
 Ser Asn Pro His Pro Leu Phe Lys Thr Phe Ile Pro Gln Met Lys Val  
 785 790 795 800  
 Glu Met Val Tyr Val Ser Gln Asn Ser Phe Phe Glu Ser Ser Ser Asp  
 805 810 815  
 Gly Arg Gly Phe Ser Ile Gly Arg Leu Leu Asn Leu Ser Ile Pro Val  
 820 825 830  
 Gly Ala Lys Phe Val Gln Gly Asp Ile Gly Asp Ser Tyr Thr Tyr Asp  
 835 840 845  
 Leu Ser Gly Phe Phe Val Ser Asp Val Tyr Arg Asn Asn Pro Gln Ser  
 850 855 860  
 Thr Ala Thr Leu Val Met Ser Pro Asp Ser Trp Lys Ile Arg Gly Gly  
 865 870 875 880  
 Asn Leu Ser Arg Gln Ala Phe Leu Leu Arg Gly Ser Asn Asn Tyr Val  
 885 890 895  
 Tyr Asn Ser Asn Cys Glu Leu Phe Gly His Tyr Ala Met Glu Leu Arg  
 900 905 910  
 Gly Ser Ser Arg Asn Tyr Asn Val Asp Val Gly Thr Lys Leu Arg Phe  
 915 920 925

<210> 13  
<211> 885  
<212> PRT  
<213> Chlamydia pneumoniae  
<400> 13

Gly Thr Tyr Thr Pro Lys Asn Thr Thr Thr Gly Ile Asp Tyr Thr Leu  
1 5 10 15  
Thr Gly Asp Ile Thr Leu Gln Asn Leu Gly Asp Ser Ala Ala Leu Thr  
20 25 30  
Lys Gly Cys Phe Ser Asp Thr Thr Glu Ser Leu Ser Phe Ala Gly Lys  
35 40 45  
Gly Tyr Ser Leu Ser Phe Leu Asn Ile Lys Ser Ser Ala Glu Gly Ala  
50 55 60  
Ala Leu Ser Val Thr Thr Asp Lys Asn Leu Ser Leu Thr Gly Phe Ser  
65 70 75 80  
Ser Leu Thr Phe Leu Ala Ala Pro Ser Ser Val Ile Thr Thr Pro Ser  
85 90 95  
Gly Lys Gly Ala Val Lys Cys Gly Gly Asp Leu Thr Phe Asp Asn Asn  
100 105 110  
Gly Thr Ile Leu Phe Lys Gln Asp Tyr Cys Glu Glu Asn Gly Gly Ala  
115 120 125  
Ile Ser Thr Lys Asn Leu Ser Leu Lys Asn Ser Thr Gly Ser Ile Ser  
130 135 140  
Phe Glu Gly Asn Lys Ser Ser Ala Thr Gly Lys Lys Gly Gly Ala Ile  
145 150 155 160  
Cys Ala Thr Gly Thr Val Asp Ile Thr Asn Asn Thr Ala Pro Thr Leu  
165 170 175  
Phe Ser Asn Asn Ile Ala Glu Ala Ala Gly Gly Ala Ile Asn Ser Thr  
180 185 190  
Gly Asn Cys Thr Ile Thr Gly Asn Thr Ser Leu Val Phe Ser Glu Asn  
195 200 205  
Ser Val Thr Ala Thr Ala Gly Asn Gly Gly Ala Leu Ser Gly Asp Ala  
210 215 220  
Asp Val Thr Ile Ser Gly Asn Gln Ser Val Thr Phe Ser Gly Asn Gln  
225 230 235 240  
Ala Val Ala Asn Gly Gly Ala Ile Tyr Ala Lys Lys Leu Thr Leu Ala  
245 250 255  
Ser Gly Gly Gly Gly Gly Asn Pro Phe Ser Asn Asn Ile Val Gln Gly  
260 265 270

Thr Thr Ala Gly Asn Gly Gly Ala Ile Ser Ile Leu Ala Ala Gly Glu  
275 280 285

Cys Ser Leu Phe Ser Glu Ala Gly Asp His Tyr Leu Asn Gly Asn Ala  
290 295 300

Ile Val Ala Thr Thr Pro Gln Thr Thr Lys Arg Asn Ser Ile Asp Ile  
305 310 315 320

Gly Ser Thr Gly Lys Asp His Glu Leu Arg Ala Ile Ser Gly His Ser  
325 330 335

Ile Phe Phe Tyr Asp Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr  
340 345 350

Asp Thr Leu Asn Leu Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr  
355 360 365

Ser Gly Ser Ile Val Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala  
370 375 380

Lys Val Ala Asp Asn Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu  
385 390 395 400

Thr Ala Gly Asn Leu Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys  
405 410 415

Gly Phe Thr Gln Thr Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr  
420 425 430

Thr Leu Lys Ala Ser Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile  
435 440 445

Pro Val Asp Ser Leu Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser  
450 455 460

Ala Ala Ser Lys Asn Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp  
465 470 475 480

Asn Gln Gly Asn Ala Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp  
485 490 495

Phe Ser Phe Val Gln Leu Ser Ala Leu Gly Thr Ala Thr Thr Thr Asp  
500 505 510

Val Pro Ala Val Pro Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln  
515 520 525

Gly Thr Trp Gly Met Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys  
530 535 540

Thr Lys Thr Ala Thr Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn  
545 550 555 560

Pro Glu Arg Gln Gly Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe  
565 570 575

WO 00/32794

Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA  
FRAGMENTS AND USES THEREOF  
Inventor(s): Andrew D. MURDIN et al.  
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Ser Asp Ile Gln Ala Ile Gln Gly Val Ile Glu Arg Ser Ala Leu Thr  
580 585 590

Leu Cys Ser Asp Arg Gly Phe Trp Ala Ala Gly Val Ala Asn Phe Leu  
595 600 605

Asp Lys Asp Lys Lys Gly Glu Lys Arg Lys Tyr Arg His Lys Ser Gly  
610 615 620

Gly Tyr Ala Ile Gly Gly Ala Ala Gln Thr Cys Ser Glu Asn Leu Ile  
625 630 635 640

Ser Phe Ala Phe Cys Gln Leu Phe Gly Ser Asp Lys Asp Phe Leu Val  
645 650 655

Ala Lys Asn His Thr Asp Thr Tyr Ala Gly Ala Phe Tyr Ile Gln His  
660 665 670

Ile Thr Glu Cys Ser Gly Phe Ile Gly Cys Leu Leu Asp Lys Leu Pro  
675 680 685

Gly Ser Trp Ser His Lys Pro Leu Val Leu Glu Gly Gln Leu Ala Tyr  
690 695 700

Ser His Val Ser Asn Asp Leu Lys Thr Lys Tyr Thr Ala Tyr Pro Glu  
705 710 715 720

Val Lys Gly Ser Trp Gly Asn Asn Ala Phe Asn Met Met Leu Gly Ala  
725 730 735

Ser Ser His Ser Tyr Pro Glu Tyr Leu His Cys Phe Asp Thr Tyr Ala  
740 745 750

Pro Tyr Ile Lys Leu Asn Leu Thr Tyr Ile Arg Gln Asp Ser Phe Ser  
755 760 765

Glu Lys Gly Thr Glu Gly Arg Ser Phe Asp Asp Ser Asn Leu Phe Asn  
770 775 780

Leu Ser Leu Pro Ile Gly Val Lys Phe Glu Lys Phe Ser Asp Cys Asn  
785 790 795 800

Asp Phe Ser Tyr Asp Leu Thr Leu Ser Tyr Val Pro Asp Leu Ile Arg  
805 810 815

Asn Asp Pro Lys Cys Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp  
820 825 830

Glu Thr Tyr Ala Asn Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala  
835 840 845

Gly Ser His Tyr Ala Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe  
850 855 860

Val Phe Glu Val Arg Gly Ser Ser Arg Ile Tyr Asn Val Asp Leu Gly  
865 870 875 880

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Gly Lys Phe Gln Phe  
885

<210> 14  
<211> 928  
<212> PRT  
<213> Chlamydia pneumoniae  
<400> 14

Met Lys Ser Ser Leu His Trp Phe Leu Ile Ser Ser Ser Leu Ala Leu  
1 5 10 15  
Pro Leu Ser Leu Asn Phe Ser Ala Phe Ala Ala Val Val Glu Ile Asn  
20 25 30  
Leu Gly Pro Thr Asn Ser Phe Ser Gly Pro Gly Thr Tyr Thr Pro Pro  
35 40 45  
Ala Gln Thr Thr Asn Ala Asp Gly Thr Ile Tyr Asn Leu Thr Gly Asp  
50 55 60  
Val Ser Ile Thr Asn Ala Gly Ser Pro Thr Ala Leu Thr Ala Ser Cys  
65 70 75 80  
Phe Lys Glu Thr Thr Gly Asn Leu Ser Phe Gln Gly His Gly Tyr Gln  
85 90 95  
Phe Leu Leu Gln Asn Ile Asp Ala Gly Ala Asn Cys Thr Phe Thr Asn  
100 105 110  
Thr Ala Ala Asn Lys Leu Leu Ser Phe Ser Gly Phe Ser Tyr Leu Ser  
115 120 125  
Leu Ile Gln Thr Thr Asn Ala Thr Thr Gly Thr Gly Ala Ile Lys Ser  
130 135 140  
Thr Gly Ala Cys Ser Ile Gln Ser Asn Tyr Ser Cys Tyr Phe Gly Gln  
145 150 155 160  
Asn Phe Ser Asn Asp Asn Gly Gly Ala Leu Gln Gly Ser Ser Ile Ser  
165 170 175  
Leu Ser Leu Asn Pro Asn Leu Thr Phe Ala Lys Asn Lys Ala Thr Gln  
180 185 190  
Lys Gly Gly Ala Leu Tyr Ser Thr Gly Gly Ile Thr Ile Asn Asn Thr  
195 200 205  
Leu Asn Ser Ala Ser Phe Ser Glu Asn Thr Ala Ala Asn Asn Gly Gly  
210 215 220  
Ala Ile Tyr Thr Glu Ala Ser Ser Phe Ile Ser Ser Asn Lys Ala Ile  
225 230 235 240

Ser Phe Ile Asn Asn Ser Val Thr Ala Thr Ser Ala Thr Gly Gly Ala  
245 250 255

Ile Tyr Cys Ser Ser Thr Ser Ala Pro Lys Pro Val Leu Thr Leu Ser  
260 265 270

Asp Asn Gly Glu Leu Asn Phe Ile Gly Asn Thr Ala Ile Thr Ser Gly  
275 280 285

Gly Ala Ile Tyr Thr Asp Asn Leu Val Leu Ser Ser Gly Gly Pro Thr  
290 295 300

Leu Phe Lys Asn Asn Ser Gly Tyr Asp Thr Ala Ala Pro Leu Gly Gly  
305 310 315 320

Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser Leu Ser Ala Leu Gly  
325 330 335

Gly Asp Ile Thr Phe Glu Gly Asn Thr Val Val Lys Gly Ala Ser Ser  
340 345 350

Ser Gln Thr Thr Thr Arg Asn Ser Ile Asn Ile Gly Asn Thr Asn Ala  
355 360 365

Lys Ile Val Gln Leu Arg Ala Ser Gln Gly Asn Thr Ile Tyr Phe Tyr  
370 375 380

Asp Pro Ile Thr Thr Ser Ile Thr Ala Ala Leu Ser Asp Ala Leu Asn  
385 390 395 400

Leu Asn Gly Pro Asp Leu Ala Gly Asn Pro Ala Tyr Gln Gly Thr Ile  
405 410 415

Val Phe Ser Gly Glu Lys Leu Ser Glu Ala Glu Ala Ala Glu Ala Asp  
420 425 430

Asn Leu Lys Ser Thr Ile Gln Gln Pro Leu Thr Leu Ala Gly Gly Gln  
435 440 445

Leu Ser Leu Lys Ser Gly Val Thr Leu Val Ala Lys Ser Phe Ser Gln  
450 455 460

Ser Pro Gly Ser Thr Leu Leu Met Asp Ala Gly Thr Thr Leu Glu Thr  
465 470 475 480

Ala Asp Gly Ile Thr Ile Asn Asn Leu Val Leu Asn Val Asp Ser Leu  
485 490 495

Lys Glu Thr Lys Lys Gly Thr Leu Lys Ala Thr Gln Ala Ser Gln Thr  
500 505 510

Val Thr Leu Ser Gly Ser Leu Ser Leu Val Asp Pro Ser Gly Asn Val  
515 520 525

Tyr Glu Asp Val Ser Trp Asn Asn Pro Gln Val Phe Ser Cys Leu Thr  
530 535 540

Leu Thr Ala Asp Asp Pro Ala Asn Ile His Ile Thr Asp Leu Ala Ala  
 545 550 555 560  
 Asp Pro Leu Glu Lys Asn Pro Ile His Trp Gly Tyr Gln Gly Asn Trp  
 565 570 575  
 Ala Leu Ser Trp Gln Glu Asp Thr Ala Thr Lys Ser Lys Ala Ala Thr  
 580 585 590  
 Leu Thr Trp Thr Lys Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Gly  
 595 600 605  
 Thr Leu Val Ala Asn Thr Leu Trp Gly Ser Phe Val Asp Val Arg Ser  
 610 615 620  
 Ile Gln Gln Leu Val Ala Thr Lys Val Arg Gln Ser Gln Glu Thr Arg  
 625 630 635 640  
 Gly Ile Trp Cys Glu Gly Ile Ser Asn Phe Phe His Lys Asp Ser Thr  
 645 650 655  
 Lys Ile Asn Lys Gly Phe Arg His Ile Ser Ala Gly Tyr Val Val Gly  
 660 665 670  
 Ala Thr Thr Thr Leu Ala Ser Asp Asn Leu Ile Thr Ala Ala Phe Cys  
 675 680 685  
 Gln Leu Phe Gly Lys Asp Arg Asp His Phe Ile Asn Lys Asn Arg Ala  
 690 695 700  
 Ser Ala Tyr Ala Ala Ser Leu His Leu Gln His Leu Ala Thr Leu Ser  
 705 710 715 720  
 Ser Pro Ser Leu Leu Arg Tyr Leu Pro Gly Ser Glu Ser Glu Gln Pro  
 725 730 735  
 Val Leu Phe Asp Ala Gln Ile Ser Tyr Ile Tyr Ser Lys Asn Thr Met  
 740 745 750  
 Lys Thr Tyr Tyr Thr Gln Ala Pro Lys Gly Glu Ser Ser Trp Tyr Asn  
 755 760 765  
 Asp Gly Cys Ala Leu Glu Leu Ala Ser Ser Leu Pro His Thr Ala Leu  
 770 775 780  
 Ser His Glu Gly Leu Phe His Ala Tyr Phe Pro Phe Ile Lys Val Glu  
 785 790 795 800  
 Ala Ser Tyr Ile His Gln Asp Ser Phe Lys Glu Arg Asn Thr Thr Leu  
 805 810 815  
 Val Arg Ser Phe Asp Ser Gly Asp Leu Ile Asn Val Ser Val Pro Ile  
 820 825 830  
 Gly Ile Thr Phe Glu Arg Phe Ser Arg Asn Glu Arg Ala Ser Tyr Glu  
 835 840 845

Ala Thr Val Ile Tyr Val Ala Asp Val Tyr Arg Lys Asn Pro Asp Cys  
850 855 860

Thr Thr Ala Leu Leu Ile Asn Asn Thr Ser Trp Lys Thr Thr Gly Thr  
865 870 875 880

Asn Leu Ser Arg Gln Ala Gly Ile Gly Arg Ala Gly Ile Phe Tyr Ala  
885 890 895

Phe Ser Pro Asn Leu Glu Val Thr Ser Asn Leu Ser Met Glu Ile Arg  
900 905 910

Gly Ser Ser Arg Ser Tyr Asn Ala Asp Leu Gly Gly Lys Phe Gln Phe  
915 920 925

<210> 15  
<211> 930  
<212> PRT  
<213> Chlamydia pneumoniae  
<400> 15

Met Lys Ile Pro Leu His Lys Leu Leu Ile Ser Ser Thr Leu Val Thr  
1 5 10 15

Pro Ile Leu Leu Ser Ile Ala Thr Tyr Gly Ala Asp Ala Ser Leu Ser  
20 25 30

Pro Thr Asp Ser Phe Asp Gly Ala Gly Gly Ser Thr Phe Thr Pro Lys  
35 40 45

Ser Thr Ala Asp Ala Asn Gly Thr Asn Tyr Val Leu Ser Gly Asn Val  
50 55 60

Tyr Ile Asn Asp Ala Gly Lys Gly Thr Ala Leu Thr Gly Cys Cys Phe  
65 70 75 80

Thr Glu Thr Thr Gly Asp Leu Thr Phe Thr Gly Lys Gly Tyr Ser Phe  
85 90 95

Ser Phe Asn Thr Val Asp Ala Gly Ser Asn Ala Gly Ala Ala Ala Ser  
100 105 110

Thr Thr Ala Asp Lys Ala Leu Ile Phe Thr Gly Phe Ser Asn Leu Ser  
115 120 125

Phe Ile Ala Ala Pro Gly Thr Thr Val Ala Ser Gly Lys Ser Thr Leu  
130 135 140

Ser Ser Ala Gly Ala Leu Asn Leu Thr Asp Asn Gly Thr Ile Leu Phe  
145 150 155 160

Ser Gln Asn Val Ser Asn Glu Ala Asn Asn Asn Gly Gly Ala Ile Thr  
165 170 175



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Thr Lys Thr Leu Ser Ile Ser Gly Asn Thr Ser Ser Ile Thr Phe Thr  
180 185 190

Ser Asn Ser Ala Lys Lys Leu Gly Gly Ala Ile Tyr Ser Ser Ala Ala  
195 200 205

Ala Ser Ile Ser Gly Asn Thr Gly Gln Leu Val Phe Met Asn Asn Lys  
210 215 220

Gly Glu Thr Gly Gly Gly Ala Leu Gly Phe Glu Ala Ser Ser Ser Ile  
225 230 235 240

Thr Gln Asn Ser Ser Leu Phe Phe Ser Gly Asn Thr Ala Thr Asp Ala  
245 250 255

Ala Gly Lys Gly Gly Ala Ile Tyr Cys Glu Lys Thr Gly Glu Thr Pro  
260 265 270

Thr Leu Thr Ile Ser Gly Asn Lys Ser Leu Thr Phe Ala Glu Asn Ser  
275 280 285

Ser Val Thr Gln Gly Gly Ala Ile Cys Ala His Gly Leu Asp Leu Ser  
290 295 300

Ala Ala Gly Pro Thr Leu Phe Ser Asn Asn Arg Cys Gly Asn Thr Ala  
305 310 315 320

Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser  
325 330 335

Leu Ser Ala Asn Gln Gly Asp Ile Thr Phe Leu Gly Asn Thr Leu Thr  
340 345 350

Ser Thr Ser Ala Pro Thr Ser Thr Arg Asn Ala Ile Tyr Leu Gly Ser  
355 360 365

Ser Ala Lys Ile Thr Asn Leu Arg Ala Ala Gln Gly Gln Ser Ile Tyr  
370 375 380

Phe Tyr Asp Pro Ile Ala Ser Asn Thr Thr Gly Ala Ser Asp Val Leu  
385 390 395 400

Thr Ile Asn Gln Pro Asp Ser Asn Ser Pro Leu Asp Tyr Ser Gly Thr  
405 410 415

Ile Val Phe Ser Gly Glu Lys Leu Ser Ala Asp Glu Ala Lys Ala Ala  
420 425 430

Asp Asn Phe Thr Ser Ile Leu Lys Gln Pro Leu Ala Leu Ala Ser Gly  
435 440 445

Thr Leu Ala Leu Lys Gly Asn Val Glu Leu Asp Val Asn Gly Phe Thr  
450 455 460

Gln Thr Glu Gly Ser Thr Leu Leu Met Gln Pro Gly Thr Lys Leu Lys  
465 470 475 480

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Ala Asp Thr Glu Ala Ile Ser Leu Thr Lys Leu Val Val Asp Leu Ser  
485 490 495

Ala Leu Glu Gly Asn Lys Ser Val Ser Ile Glu Thr Ala Gly Ala Asn  
500 505 510

Lys Thr Ile Thr Leu Thr Ser Pro Leu Val Phe Gln Asp Ser Ser Gly  
515 520 525

Asn Phe Tyr Glu Ser His Thr Ile Asn Gln Ala Phe Thr Gln Pro Leu  
530 535 540

Val Val Phe Thr Ala Ala Thr Ala Ala Ser Asp Ile Tyr Ile Asp Ala  
545 550 555 560

Leu Leu Thr Ser Pro Val Gln Thr Pro Glu Pro His Tyr Gly Tyr Gln  
565 570 575

Gly His Trp Glu Ala Thr Trp Ala Asp Thr Ser Thr Ala Lys Ser Gly  
580 585 590

Thr Met Thr Trp Val Thr Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg  
595 600 605

Ala Ser Val Val Pro Asp Ser Leu Trp Ala Ser Phe Thr Asp Ile Arg  
610 615 620

Thr Leu Gln Gln Ile Met Thr Ser Gln Ala Asn Ser Ile Tyr Gln Gln  
625 630 635 640

Arg Gly Leu Trp Ala Ser Gly Thr Ala Asn Phe Phe His Lys Asp Lys  
645 650 655

Ser Gly Thr Asn Gln Ala Phe Arg His Lys Ser Tyr Gly Tyr Ile Val  
660 665 670

Gly Gly Ser Ala Glu Asp Phe Ser Glu Asn Ile Phe Ser Val Ala Phe  
675 680 685

Cys Gln Leu Phe Gly Lys Asp Lys Asp Leu Phe Ile Val Glu Asn Thr  
690 695 700

Ser His Asn Tyr Leu Ala Ser Leu Tyr Leu Gln His Arg Ala Phe Leu  
705 710 715 720

Gly Gly Leu Pro Met Pro Ser Phe Gly Ser Ile Thr Asp Met Leu Lys  
725 730 735

Asp Ile Pro Leu Ile Leu Asn Ala Gln Leu Ser Tyr Ser Tyr Thr Lys  
740 745 750

Asn Asp Met Asp Thr Arg Tyr Thr Ser Tyr Pro Glu Ala Gln Gly Ser  
755 760 765

Trp Thr Asn Asn Ser Gly Ala Leu Glu Leu Gly Gly Ser Leu Ala Leu  
770 775 780

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Tyr Leu Pro Lys Glu Ala Pro Phe Phe Gln Gly Tyr Phe Pro Phe Leu  
785 790 795 800  
Lys Phe Gln Ala Val Tyr Ser Arg Gln Gln Asn Phe Lys Glu Ser Gly  
805 810 815  
Ala Glu Ala Arg Ala Phe Asp Asp Gly Asp Leu Val Asn Cys Ser Ile  
820 825 830  
Pro Val Gly Ile Arg Leu Glu Lys Ile Ser Glu Asp Glu Lys Asn Asn  
835 840 845  
Phe Glu Ile Ser Leu Ala Tyr Ile Gly Asp Val Tyr Arg Lys Asn Pro  
850 855 860  
Arg Ser Arg Thr Ser Leu Met Val Ser Gly Ala Ser Trp Thr Ser Leu  
865 870 875 880  
Cys Lys Asn Leu Ala Arg Gln Ala Phe Leu Ala Ser Ala Gly Ser His  
885 890 895  
Leu Thr Leu Ser Pro His Val Glu Leu Ser Gly Glu Ala Ala Tyr Glu  
900 905 910  
Leu Arg Gly Ser Ala His Ile Tyr Asn Val Asp Cys Gly Leu Arg Tyr  
915 920 925  
Ser Phe  
930

<210> 16  
<211> 293  
<212> PRT  
<213> Chlamydia pneumoniae  
<400> 16

Met Leu Ser Ser Leu Ile Arg Asp Ser Phe Pro Leu Leu Ile Leu Leu  
1 5 10 15  
Pro Thr Phe Leu Ala Ala Leu Gly Ala Ser Val Ala Gly Gly Val Met  
20 25 30  
Gly Thr Tyr Ile Val Val Lys Arg Ile Val Ser Ile Ser Gly Ser Ile  
35 40 45  
Ser His Ala Ile Leu Gly Gly Ile Gly Leu Thr Leu Trp Ile Gln Tyr  
50 55 60  
Lys Leu His Leu Ser Phe Phe Pro Met Tyr Gly Ala Ile Val Gly Ala  
65 70 75 80  
Ile Phe Leu Ala Leu Cys Ile Gly Lys Ile His Leu Lys Tyr Gln Glu  
85 90 95

Arg Glu Asp Ser Leu Ile Ala Met Ile Trp Ser Val Gly Met Ala Ile  
100 105 110

Gly Ile Ile Phe Ile Ser Arg Leu Pro Thr Phe Asn Gly Glu Leu Ile  
115 120 125

Asn Phe Leu Phe Gly Asn Ile Leu Trp Val Thr Pro Ser Asp Leu Tyr  
130 135 140

Ser Leu Gly Ile Phe Asp Leu Leu Val Leu Gly Ile Val Val Leu Cys  
145 150 155 160

His Thr Arg Phe Leu Ala Leu Cys Phe Asp Glu Arg Tyr Thr Ala Leu  
165 170 175

Asn His Cys Ser Val Gln Leu Trp Tyr Phe Leu Leu Leu Val Leu Thr  
180 185 190

Ala Ile Thr Ile Val Met Leu Ile Tyr Val Met Gly Thr Ile Leu Met  
195 200 205

Leu Ser Met Leu Val Leu Pro Val Ala Ile Ala Cys Arg Phe Ser Tyr  
210 215 220

Lys Met Thr Arg Ile Met Phe Ile Ser Val Leu Leu Asn Ile Leu Cys  
225 230 235 240

Ser Phe Ser Gly Ile Cys Ile Ala Tyr Cys Leu Asp Phe Pro Val Gly  
245 250 255

Pro Thr Ile Ser Leu Leu Met Gly Leu Gly Tyr Thr Ala Ser Leu Cys  
260 265 270

Val Lys Lys Arg Tyr Asn Pro Ser Thr Pro Ser Pro Val Ser Pro Glu  
275 280 285

Ile Asn Thr Asn Val  
290